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AJ243224 Homo sapi
AJ243212 Homo sapi
AJ297935 Homo sapi
AF159456 Homo sapi
AC131207 Homo sapi
AF064259 Strongylo
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Z22968 H.saplens m
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AJ000342 Homo sap1
Y14953 Geodia cydo
AF043112 Oryctolag
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AB005909 Mus muscu
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misc_feature 11121432 /note="Region: scavenger receptor cysteine-rich domain SRCR 4" 1753 misc_feature 14331753 /note="Region: scavenger receptor cysteine-rich domain hisc_feature"	2074 Region: scavenger receptor cysteine-rich	SKCK 0" 20752395 Anote="Region: scavenger receptor cysteine-rich domain epcp 7"	misc_feature 5702710 //note="Region: scavenger receptor cysteine-rich domain corp at a corp a	misc_feature 27113025 //note="Region: scavenger receptor cysteine-rich domain	<pre>misc_feature 30263118 /note="Region: interdomain segment"</pre>	misc_feature 3119. 3433 /note="Region: scavenger receptor cysteine-rich domain SRCR 10"	misc_feature 3434. 3754 /note="Region: scavenger receptor cysteine-rich domain cpc 11"	misc_feature 3755. 4063 /note="Region: scavenger receptor cysteine-rich domain	misc_feature 4043 //orde="Beaing connecting pertide"	transmembra		4388. 4579 4456. 4461	50. 919	Alignment Scores: 0 Length: 4579 Pred. No.:	Matches: Conservative: C Mismatches:			Oy 1 MetMetLeuProGlnAsnSerTrpHisIleaspPheGlyArgCysCysHisGlnAsn 20	Oy 21 LeupheSerAlaValVhrCysIleLeuLeuLeuAsnSerCysPheLeuIleSerSer 40	Oy 41 PheAsnGlyThrAspLeuGluLeuArgLeuValAsnGlyAspGlyProCysSerGlyThr 60	61	206 GTGGGAGGTGAAATTCCAGGGACAGTGGGGGGACACTGTGTGGGTGG	Oy 81 AlaserThreValValVasivySthLeuglyCystrOffreatrieAlameternerigen grie 100   1	Oy 101 GlyGlnalaValThrArgHisGlyLysIleTrpLeuAspAspValSerCysTyrGlyAsn 120
z	ACCESSION AF264014 VERSION AF264014.1 GI:9652086 KEYWORDS Homo sapiens.	_	REFERENCE 1 (bases 1 to 4579) AUTHORS Gronlund,J., Vitved,L., Lausen,M., Skjodt,K. and Holmskov,U. TITLE Cloning of a novel scavenger receptor cysteine-rich type I		FUBMED 11086079  REFERENCE 2 (bases 1 to 4579) AUTHORS Groenlund, J., Vitved, L., Lausen, M., Skjodt, K. and Holmskov, U.		al blology, university of Southern Winsloewparken 21.1, Odense 5000, Qualifiers	source 1. 4579 /organism="Homo sapiens" /db_xref="taxon:9606"	/chromosome="12" /map="12q13.3"	5'UTR 1. 25 CDS 26. 4387	/codon_start=1 /product="scavenger receptor cysteine-rich type 1 protein	M160 precursor" /protein_id="ARF91396.1" /db_xref="G1:9652087"		NNSCSGRVEYKFOERMGTICDDGWNI.NTAAVVCRQLGCPSFISSGVVNSFAVLRPIW LIDDILCQGROELALMNCRHRGWGNHDCSHDEDVTTGYDSSDLELRLVGGTNRCWGRVE 1.KTOREWGTVCHHKNNNAARDVCRQLGCGTALHFRGLPHLOSGSDYVWLDGYSCSGN	ESFLMDCRHSGTVNFDCLHQNDVSVICSDGADLELRLADGSNNCSGRVBYRIHEDWWT ICODWWRNDSALVCKOLGCPFSVFGSRRARCSNERNDIN WIN SISCYGNESALMDCTY DGRARRTCFRRSDAGVICSDRADLDLRLVGAHSPCYGRLBYKYGGBWGTVCHDRWSTR	NAAVYCKQLGGGRPMHYEGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCV HREDVIVTGSGDATWGLRIVGGSRIRCSGRIEVFGGRWGYCODGWRAKAAAVYCSGUL	DCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGNNCSHSEDVGVIC SDASDWEIRIVGGSSRCAGKVEVVNGAVGILCANGWGNNIAEVVCRQLEGGSAIRVS STATINGTHY ANALOG THE TOTAL	GADMPCSGRVEVKHADTMRSVCGCTGGRASIMULIRMEMRUTAGENGERGERU GADMPCSGRVEVKHADTWRSVCDSDFSLHAANDCTGELNGGDAISLSVGDHFGKONGL TWAEKFQCGGSETHLALCPIYOOHPEDTCIHGREVGVVCSRYTDVRLVNGKSQCDGQVE INVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGN	ESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALIC LEDKRLKLVDGDSRCAGKVETYHDGFWGTICDDGWTLSDAHVYCQKLGCGVAFNATVS AHFGEGSGPINLDDLNCTGMESHLWQCPSRCWGOHDCRHKEDAGVICSEFTALRLYSE TPTFACAGAFFYRTWATWGSYCKRNTTTAAAGVCROGGENGVYSLAPLSKTGSGF	MWYDDIQCPKTHISINQCLSAPWERRISSTAEETWITCEDRIRVRGGDTECSGRVEIW HAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRASFGGGTGTIWLDDWRCKGNES FUNDGHRAPWGSDGGHREDAGVRGSQQLKGLAFALILSSIFGLLLDVLFIL FUNDGHRAPWGSDGGRREDAGVRGSQQLKGLAFALILSSIFGLLLDVLFIL	ASDTSLIGVLPASEATK" sig_peptide 26151 misc_feature 152469	/note SRCR	<pre>misc_feature 470 790 //onte="Region: scavenger receptor cysteine-rich domain SRCR 2"</pre>	<pre>misc_feature 7911111 /note="Region: scavenger receptor cysteine-rich domain SRCR 3"</pre>

Tue

	481 Alah      466 GCTC	-	F26 TGTC	521 LysP       586 AAGC	541 AspA		561 GLYL        706 GGAA			601 GlnG	, ,	621 Cyss       886 TGTA	641 GlyT		661 SerC        006 TCAT	681 IleC		701 GLYE	126 GGAA 721 Meta	1111 2186 ATGA	741 ArgG		761 G1yG 1111	ب د - د	366 TTAA	801 ASPM			486 GATT
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GGAAAA	GlnHis	CAACAC	TyrGly        TACGGT	ValGlu 	Thrala	ACTGCT	ValAsn	GTTAAT	GluLeu.         GAGTTG	GluAsp	GAGGAT	Thrasn	HisHis	CACCAT	AlaLeu	GCACII	GLYVAL         GGTGTC	AsnPhe	AATTT	Gluren	Glugla	GAACAG	LysGln	AAGCAG	AlaArg	GVSThr	TGCACA	Cysser	TGTTCT
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GACAAGCCGTGACTAGACATGGAAAAATTTGGCTTGATGAT	luSerAla	GTCAGC	GluaspvalGlyv 	AsnAsnSer	pAspGly	GATGATGG	SerPhelleSerSerGlyValValAsnSerProAlaValLeuArgProlle	TTTTAT	ASpIleLeuCysGlnGlyAsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTrpGly 	AsnHisAspCysSerHisAsnCluAspValThrLeuThrCysTyrAspSerSerAspLeu	TCATGA	GluLeuArgLeuValGlyGlyThrAsnArgCysMetGlyArgValGluLeuLysIleGln []	yArgTri		LysGlnLeuGlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGlnSerGly	ocasil.	eraspyalvalitpuelusspelyvalsertysserelyaspeluserpnele 	SArgHis		CysSerAspGlyA	gValGlu	AGAGTAGAG	GluGlnAlaLeuValValCysLysGlnLeuGlyCysProPheSerValPheGlySerArg	ACAAGC	ArgalaLysProSerAsnGlualaArgaspileTrpilleAsnSerileSerCysThrCly	TGLUSE		gSerAsi	
326 GG	<u> </u>		141 Gly 11 446 GA	161 ASI		11 566 GA			221 AS  	241 AS	746 AA	261 G1		<b>–</b> о	301 Ly		v — F	o -	   1046 TG	361 Cy				1226 GA	421 Ar	<u> </u>		461 Ar	1406 AG
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Bukaryotas; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3670)

Shinkets; R.A., Fernandes, E., Herrmann, J.L., Liu, X., Yang, M. and
Boldog, F.L.

Secreted human proteins, polynucleotides encoding them and method
of using the same
Patent; WO 0119856-A 15 22-MAR-2001;
Curagen Corporation (US)
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Sequence 15 from Patent W00119856.
AXI33829
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/db_xref="taxon:9606"
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AsncysGlyAspAlaileSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeu 856 	17	88	18	TyrthraspvalargleuvalasnGlyLysSerGlnCysAspGlyGlnValGluIleAsn 916 			Leuvysargeinebbervystylinerdebesettiinen hyvytystytytostytylinen herioty (	.10	GAAAGAAGTGTTCGTGTGGGGGACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTG 20	AspAsnCysGlnMetThrValleuGlYAlaPrOProCysIleHisGlyAAnThrVallser 996 			ProTyrLeuSeralaValProGluGlySerAlaLeuIleCysLeuGjuAspLysArgLeu 1036 	UCAIAIIIGICIGCAGIICCAGGAGGGCGGGGGGGGGGGG	ATGLEWATABOLYARDSETALGVYSALGALYALGYGALALLEETYTTESSELYTETE TO CCCCTAGTGGGTGGGGGGGGGCGCTGTGCCGGGGGGGGGG	TrpGlyThr11eCysAspAspGlyTrpAspLeuSerAspAlaHisValValCysGlnLys 107	regescaccarcrereareacescressaccresserscccacerescressers 234	LeuGlyCysGlyValAlaPheAsnAlaThrValSerAlaHisPheGlyGluGlySerGly 1096 	ProlleTrpLeuAspAspLeuAsnCysThrGluyThrGluSerHisLeuTrpGlnCysPro	CCCATCTGGCTGGATGACCTGCACAGGAATGGAGTCCCCACTTGTGGCAGTCCCCT	SerargGlyTrpGlyGlnHisAspCysArgHislysGluAspAldGlyVallieCysSer 113b 	GluPheThralaLeuArgLeuTyrSerGluThrGluThrGluLSerCysAlaGlyArgLeu 1156 	GluvalpheryrasnGlyThrTrpGlySerValGlyargAsnIleThrThrAlaile 1176 	AlaGlyIleValCysArgGlnLeuGlyCysGlyGluAsnGlyValValSerLeuAlaPro 1196 	LeuSerLysThrGlySerGlyPheMetTrpValAspAsp1leGlnCysProLysThrHis 1216
837	857	877	1742	897	917	1862	1922	957	1982	977	997	2102	1017	2012	103/	1057	2282	1077	1097	2402	1117	1137	1157 2582	1177	1197
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ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S.,
Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK058038 2249 bp mRNA linear PRI 31-OCT-2001 Homo sapiens cDNA FLJ25309 fis, clone SYN00985, highly similar to Homo sapiens scavenger receptor cysteine-rich type 1 protein MIG0
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AK058038.1 GI:16554040
Oligo capping; fis (full insert sequence).
Homo sapiens synovial membrane (knee) cDNA to mRNA, clone_lib:SYN
clone:SYN00985.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                              Direct Submission

L Submitted (24-C77-2001) Sumio Sugano, Institute of Medical Science, Direct Submission

L Submitted (24-C77-2001) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:3-5449-5416)

REA:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: Rab; clone selection for full insert sequencing: Rab and Helix Research Institute.
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Matches:
Conservative:
Mismatches:
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Sugano, S. and Suzuki, Y.
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          CysLeuGluAspLysArgLeuArgLeuValAspGlyAspSerArgCysAlaGlyArgVal
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DDLICNGNESALWNCKHQGWGKHNCDHAABDAGVICSKGADLSLRLVDGVTECSGRLEV
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Submitted (14-JUN-1993) Kingsley K.J. Micklem, Nuffield Department
of Pathology, University of Oxford, Level 1, Maternity Block, John
Radcliffe, Hospital, Headington, Oxford, Ox3 9DU, United Kingdom
Z. Poases 1 to 3786)
Law, S.K., Micklem, K.J., Shaw, J.M., Zhang, X.P., Dong, Y., Willis, A.C.
and Mason, D.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new macrophage differentiation antigen which is a member of the
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               CATCTGCCCCTCAGAGTTTCAACCAGAAGGAGGGGTTCTCTCGCGGAGAATTTATTCCAT 1922
LeuaspaspmetargCysLysGlyasnGluSerPheLeuTrpaspCysHisalaLysPro 1329
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                                                                                                                  LeuLysSerLeuAsnAlaSerSerGlyHisLeuAlaLeuIleLeuSerSerIlePheGly 1369
                                                                                                                                1983 CCCAACCATGGTTGTGAAGATGCTAGCGACACATCGCTGTTGGGAGTTCTTCCTGCCTCT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Micklem,K.K.
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Eur. J. Immunol. 23 (9), 2320-2325 (1993)
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Lys 562       AAG 821	G1y 582 AGC 881	(G1y 602       GGA 941	Ser 622 AAG 1001	Tyr 642	Cys 662       TGT 1121	Cys 682      NGT 1181	Lys 702 ACA 1241	Asn 722 AAA 1301	JGlu 742	/G1y 762 AAT 1421	Asn 782 TAT 1481	Met 802 ::: :ATT 1541	oser 822 · · · · · · · · · · · · · · · · · ·	ille 842 ::: rGrc 1661	sPhe 862       \rrc 1721	ASP 882 AGGA 1781	JLeu 902       TTG 1841	92
3 ValSerCysIleGlyAsnGluSerAsnIleTrpAspCysGluHisSerGlyTrpGlyLys :::	3 HisasnCysValHisargGluaspValIleValThrCysSerGlyAspAlaThrTrpGly 	3 LeuargleuvalgiygiyserasnargCysserGiyargLeuGiuvalTyrbheGinGiy 	3 ArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaAlaValValCysSer 	3 GlnLeuAspCysProSerSerIleIleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyr 	3 GlyLysileTrpLeuAspAspValSerCysAspGlyAspGlùSerAspLeuTrpSerCys 	3 argasnSerGlyTrpGlyasnaspCysSerHisSerGluaspValGlyValIleCys :::::	3 SerAspAlaSerAspWetGluLeuArgLeuValGlyGlySerSerArgCysAlaGlyLys 	3 ValGluValAsnValGlnGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGlyMe            :::    :::    :::	3 IlealaGluValValValCysArgGlnLeuGluCysGlySerAlaIleArgValSerArgGlu 	3 ProHisPheThrGluargThrLeuHisIleLeuMetSerAsnSerGlyCysThrGlyGly 	m 0	3 MetGlualaSerLeuIleCysSerAlaHisArgGlnProArgLeuValGlyAlaAspWet         :::	3 ProcysSerGlyArgValGluValLysHisAlaAspThrTrpArgSerValCysAspSer	ъ с	3 SerLeuSerValGlyAspHisPheGlyLySGlyAsnGlyLeuThrTrpAlaGluLySPhe	3 GlnCysGluGlySerGluThrHisLeuAlaLeuCySProIleValGlnHisProGluAs	3 ThrCysIleHisSerArgGluValGlyValValCysSerArgTyrThrAspValArgLeP 	m
y 54 b 76	y 56	y 58	y 600:	y 62: b 100:	y 64.	y 66 b 112	у 68 b 118	y 70 b 124	y 72. b 130	y 74 b 136	y 76: b 142:	y 78 b 148	y 80 b · 154	y 82. b 160	y 843 b 1662	y 86. b 172	Oy 88 Db 178	6
oy Dp	O.y Db	9 9	S G	P Q	S S	S S	OY Db	Q D	Qy Db	oy Dp	g G	ę P	Oy Dp	S G	o G	S S	S G	õ

1142 1222 1242 1083 PheAsnAlaThrValSerAlaHisPheGlyGluGlySerGlyProIleTrpLeuAspAsp 1102 2441 1162 2621 1202 2741 2201 2321 2381 2561 2801 2861 2921 HisalaGlySerTrpGlyThrValCysAspAspSerTrpAspLeuAlaGluAlaGluVal 1282 SerLeuCysAspThrHisTrpAspProGluAspAlaArgValLeuCysArgGlnLeuSer 942 |||||||||||||| | TCCCTCTGTAACTCTCACTGGGACATAGAAGATGCCCATGTTCTTTGCCAGCAGCAGCTTAAA 1961 2081 SerArgCysAlaGlyArgValGluIleTyrHisAspGlyPheTrpGlyThrIleCysAsp 1062 AspGlyTrpAspLeuSerAspAlaHisValValCysGlnLysLeuGlyCysGlyValAla 1082 1243 GluAspArgIleArgValArgGlyGlyAspThrGluCysSerGlyArgValGluIleTrp 1262 ValLeuGlyAlaProProCys1leHisGlyAsnThrValSerVallleCysThrGlySer 1002 LeuThrGlnProLeuPheProCysLeuAlaAsnValSerAspProTyrLeuSerAlaVal 1022 2862 GACAACAAGATAAGAACTTCAGGAAGCCACTTCCTGTTCTGGACGTGTGGAAGTTCTG CysGlyThrAlaLeuSerThrThrGlyGlyLysTyrIleGlyGluArgSerNalArgVal 2082 GCTCTAGGTGCTTCATTATGTCCTTCAGAGCAAGTGGCCTCTGTAATCTGCTCAGGAAAC 2142 CAGTCCCAAACACTGTGGAATTCATCATCTTTGGGCCCAAAGGCCTACCATT GlnLeuGlyCysGlyGluAsnGlyValValSerLeuAlaProLeuSerLysThrGlySer 1223 LeuSerAlaProTrpGluArgArgIleSerSerProAlaGluGluThrTrpIleThrCys 2802 CCATCATCTCCATGGGAGAGAGACTGGCCACCCCTCGGAGGAGACCTGGATCACATGT TrpGlyHisArgPheHisCysLeuGlyAsnGluSerLeuLeuAspAsnCysGlnMetThr 1962 1003 2262 2382 1183 1263 1842 1902 1023 2202 1043 1063 2322 943 963 983 923 qq q qq g g qq q g g g δ g Ω ò à ò à ò g g qq ò g g à g ò ŏ ò ò δ ò δ ò

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                                                                                                                                                                                                                                                           VICRELOCGTVVSILGGAHFGEGNGQIMAEEPQCEGHESHLSLCPVAPRPEGTCSHSR
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DDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEV
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Law S.K., Micklem, K.J., Shaw, J.M., Zhang, X.P., Dong, Y., Willis, A.C. and Mason, D.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-JUN-1993) Kingsley K.J. Micklem, Nuffield Department of Pathology, University of Oxford, Level 1, Maternity Block, John Radcliffe, Hospital, Headington, Oxford, OX3 9DU, United Kingdom Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                      3447 GCTGATTTCAGTGCTGCTGAACTAATTTCTGTGTCTAAATTTCTTCCTATTTCTGGAATG 3506
                                     ValCysGlnGlnLeuGlyCysGlySerAlaLeuAlaAlaLeuArgAspAlaSerPheGly 1302
                                                                                                                                                                                                                                                                                                                                          SerGlyHisLeuAlaLeuIleLeuSerSerIlePheGlyLeuLeuLeuValLeuPhe 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3393 CTGAATGCAGATGATCTGGACCTAATGAATTCCTCAGAAAAT-----TCCCATGAGTCA 3446
                                                                                                                GlnGlyThrGlyThrIleTrpLeuAspAspMetArgCysLysGlyAsnGluSerPheLeu 1322
                                                                                                                                   ValArgCysSerGlyGlnSerLeuLys-------SerLeuAsnAlaSer 1356
                                                                                                                                                                                                                                                                                                                                                                                                                 Ile-----LeuPheLeuThrTrpCysArgValGlnLysGlnLysHisLeuProLeuArg 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValSerThrArgArgArgGlySerLeuGluGluAsnLeuPheHisGluMetGluThrCys 1414
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CATGGAGGTTCCTGGGGGACAGTGTGATGACTCTTGGGACTTGGACGATGCTCAGGTG 2981
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GTTTCCTCAAGAGGAGAGAACTTAGTCCCACCAAATTCAATACCGGGAGATGAATTCTTGC
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102. .3452
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antigen; antigen M130.
Homo sapiens.
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AspGlyTrpAspLeuSerAspAlaHisValValCysGlnLysLeuGlyCysGlyValAla 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheAsnalaThrValSerAlaHisPheGlyGluGlySerGlyProIleTrpLeuAspAsp 1102
           ValLeuGlyAlaProProCysIleHisGlyAsnThrValSerValIleCysThrGlySer 1002
                                                                                                                                                                                                                                                                                            1082 GCTCTAGGTGCTTCATTATGTCCTTCAGAGCAAGTGGCCTCTGTAATCTGCTCAGGAAAC 2141
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                                                                                                                                SerLeuCysAspThrHisTrpAspProGluAspAlaArgValLeuCysArgGlnLeuSer 942
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                                           ThrCysIleHisSerArgGluValGlyValValCysSerArgTyrThrAspValArgLeu 902
GlnCysGluGlySerGluThrHisLeuAlaLeuCysProIleValGlnHisProGluAsp 882
                                                                                      ValAsnGlyLysSerGlnCysAspGlyGlnValGluIleAsnValLeuGlyHisTrpGly
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QTLSSCNSSSLGPTRPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
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PAVWQCKHHEWGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRLLGKV
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AFREAEFGQGTGPIWLNEVKCKGNESSLWDCPARRWGHSECGHKEDAAVNCTDISVQK
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AGSGRIWMDHVSCRGNESALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLIRGG
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222. .3569
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/evidence.experimental
                              /product="M130 antigen cytoplasmic variant/
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/db_xref="G1:312146"
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Submitted (14-0701-1993) Kingsley K.J. Micklem, Nuffield Department
of Pathology, University of Oxford, Level 1, Maternity Block, John
Radcliffe, Hospital, Headington, Oxford, Ox3 9DU, United Kingdom
C Daws.K., Micklem, K.J., Shaw,J.M., Zhang,X.P., Dong,Y., Willis,A.C.
and Mason,D.Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Micklem,K.K.
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                                                                       GACAACAAGATAAGACTTCAGGAAGGACCCACTTCCTGTTCTGGACGTGTGGAGATCTGG
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/cell_type="Macrophage"
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antigen; antigen M130.
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O.y	543	ValSerCysileGlyAsnGluSerAsnileTrpAspCysGluHisSerGlyTrpGlyLys 562 :::	
oy Op	563	HisasnCysvalHisargGludspvalIlevalThrCysSerGlyAspalaThrTrpGly 582 	
o S	583	LeuargLeuValGlyGlySerAsnargCysSerGlyargLeuGluValTyrPheGlnGly 602 	
Oy Dp	603	ArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaAlValValCysSer 622 	
Qy Dp	623	GlnLeuAspCysProSerSerIleIleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyr 642 	
Oy Dp	643 1062	GlyLysileTrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCys 662 	
oy Ob	663	ArgAsnSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAspValGlyValIleCys 682 :::::               :::         :::	
oy Op	683 1182	SerAspalaserAspMetGluLeuArgLeuValGlyGlySerSerArgCysAlaGlyLys 702                 :::	٠
oy Dp	703	ValdiuValasnValdinGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGlyMetAsn 722. 	
Oy Dp	723 1302	IleAlaGluValValCysArgGlnLeuGluCysGlySerAlaIleArgValSerArgGlu 742	
oy G	743	ProHisPheThrGluArgThrLeuHisIleLeuMetSerAsnSerGlyCysThrGlyGly 762 ::: ::: :::	٠.
oy op	763	GlualaSerLeuTrpAspCysIleargTrpGluTrpLysGlnThrAlaCysHisLeuAsn 782 	
qa	783	MetGlualaserLeuIleCysseralaHisArgGlnProArgLeuValGlyAlaAspMet 802 	
Oy Dp	803 1542	ProcysSerGlyArgValGluValLysHisAlaAspThrTrpArgSerValCysAspSer 822 	
Oy Dp	823 1602	ASPPheSerLeuHisAlaAlaAsnValLeuCysArgGluLeuAsnCysGlyAspAlaIle 842 	
λ̈́o	843	SerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThrTrpAlaGluLysPhe 862    :::	

ValLeuGlyAlaProProCysIleHisGlyAsnThrValSerValIleCysThrGlySer 1002 1003 LeuThrGlnProLeuPheProCysLeuAlaAsnValSerAspProTyrLeuSerAlaVal 1022 2201 10082 GCTCTAGGTGCTTCATTATGTCCTTCAGAGCAAGTGGCCTCTGTAATCTGCTCAGGAAAC 2141 AspGlyTrpAspLeuSerAspAlaHisValValCysGlnLysLeuGlyCysGlyValAla 1082 1083 PheAsnAlaThrValSerAlaHisPheGlyGluGlySerGlyProIleTrpLeuAspAsp 1102 KeuAsnCysThrGlyThrGluSerHisLeuTrpGlnCysProSerArgGlyTrpGlyGln 1122 1163 ThrTrpGlySerValGlyArgArgAsnIleThrThrAlaIleAlaGlyIleValCysArg 1182 1662 TCTATCCTGGGGGGGGTCACTTTGGAGAGGGAAATGGACAGATCTGGGCTGAAGAATTC 1721 TrpGlyHisArgPheHisCysLeuGlyAsnGluSerLeuLeuAspAsnCysGlnMetThr 982 CysGlyThrAlaLeuSerThrThrGlyGlyLysTyrIleGlyGluArgSerValArgVal 2322 GACAGCTGGGACCTGAGTGATGCCCACGTGTTGCAGACAGCTGGGCTGTGGAGAGGCC 863 1722 1782 943 1962 696 2022 983 2202 1063 2382 1103 2442 1123 2502 1143 2562 1183 2682 1023 2622 883 οy g pp Dp ò g οy d δ g οy qq ò Dp Qy 9 9 9 9 g g g δ g δ g δ Dp ŏ à g ò ò

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LLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYREMNSCLNADDLDLMNSSGGHS
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VLCRELQCGTVVSILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSHSR
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ELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTG
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                                                                                                                                      /translation="MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDK
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/db_xref="G1:312148"
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Submitted (14-JUN-1993) Kingsley K.J. Micklem, Nuffield Department
of Pathology, University of Oxford, Level 1, Maternity Block, John
Radcilife, Hospital, Headington, Oxford, Ox3 9DU, United Kingdom
2 (bases 1 to 3802)
Law, S.K., Micklem, K.J., Shaw, J.M., Zhang, X.P., Dong, Y., Willis, A.C.
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                    GACAACAAGATAAGACTTCAGGAAGGACCACTTCCTGTTCTGGACGTGTGGAGATCTGG
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                                                                             GluAspArgIleArgValArgGlyGlyAspThrGluCysSerGlyArgValGluIleTrp
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 3802)
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H.sapiens mRNA for M130 antigen extracellular variant.
Z22971
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Eur. J. Immunol. 23 (9), 2320-2325 (1993)
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/organism="Homo sapiens"
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Oy Dp	483 582	SerProCysTyrGlyArgLeuGluValLysTyrGlnGlyGluTrpGlyThrValCysHis 502 :::	
9 9	503	LysPro 52 AGTGCT 70	
Oy Dp	523	MethisValPheGlyMetThrTyrPheLysGlualaSerGlyProIleTrpLeuAspAsp       542         :::	
oy Op	543	ValSerCysIleGlyAsnGluSerAsnIleTrpAspCysGluHisSerGlyTrpGlyLys 562 :::	
Oy Db	563 822	HisasncysvalHisargGluaspvalIlevalThrCysSerGlyaspalaThrTrpGly 582 	
op Op	583	LeuArgLeuValGlyGlySerAsnArgCysSerGlyArgLeuGluValTyrPheGlnGly 602 	
Oy Dp	603	ArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaAlaAlValValCysSer 622 	
Oy Db	623	GInLeuAspCysProSerSerIleIleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyr 642 	
Qy Dp	643	GlyLysileTrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCys 662	
Oy Dp	663	ArgasnSerGlyTrpGlyasnasnaspCysSerHisSerGluaspValGlyValIleCys 682 :::::	
Qy Dp	683	SeraspalaseraspMetGluLeuargLeuValGlyGlySerserargCysalaGlyLys 702                :::	
Oy Dp	703	ValGluValasnValGlnGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGlyMetAsn 722 	
Oy Dp	723	IlealaGluValValCysArgGlnLeuGluCysGlySerAlaIleArgValSerArgGlu 742	
9. Pb	743	ProHisPheThrGluargThrLeuHisIleLeuMetSerasnSerGlyCysThrGlyGly 762 ::: :::	
Oy Oy	763	GlualaserLeuTrpaspCysIleargTrpGluTrpLysGlnThralaCysHisLeuasn 782                         GaaaCTTCTCTTTGGGACTGCAAGAACTGGCAATGGGGTGGACTTACCTGTGATCACTAT 1481	
Qy Db	783	MetGlualaSerLeulleCysSeralaHisargGlnProArgLeuValGlyalaAspMet       802	
Oy Db	803	ProCysSerGlyArgValGluValLysHisAlaAspThrTrpArgSerValCysAspSer 822 	
Q Q	823 1602	ASPPHESErLeuHisAlaalaAsnValLeuCySArgGluLeuAsnCysGlyAspAlaIle 842 	

1069 2441 1089 1009 2261 2321 2501 2561 AspalaGlyValIleCysSerGluPheThrAlaLeuArgLeuTyrSerGluThrGluThr 1149 2141 2201 CysLeuAlaAsnValSerAspProTyrLeuSerAlaValProGluGlySerAlaLeuIle 1029 HisPheGlyGluGlySerGlyProlleTrpLeuAspAspLeuAsnCysThrGlyThrGlu 1109 SerHisLeuTrpGlnCysProSerArgGlyTrpGlyGlnHisAspCysArgHisLysGlu 1129 2621 2681 1721 1961 2021 2081 1170 ArgAsnIleThrThrAlaIleAlaGlyIleValCysArgGlnLeuGlyCysGlyGluAsn 1189 696 686 1842 TTAATTGGTTCTTATACTGTGAAAGGGACAGGGTTAGGGAGTCATAGCTGTCTTTTTCTA 1901 949 862 968 909 2082 CCAGGAGGAGCACGTTTGGAAAAGGAAATGGTCAGATCTGGAGGCATATGTTTCACTGC 970 LeuGlyAsnGluSerLeuLeuAspAsnCysGlnMetThrValLeuGlyAlaProProCys 990 IleHisGlyAsnThrValSerVallleCysThrGlySerLeuThrGlnProLeuPhePro SerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThrTrpAlaGluLysPhe GlnCysGluGlySerGluThrHisLeuAlaLeuCysProIleValGlnHisProGluAsp 950 ThrGlyGlyLysTyrIleGlyGluArgSerValArgValTrpGlyH1sArgPheH1sCys 2202 CCTTCAGAGCAAGTGGCCTCTGTAATCTGCTCAGGAAACCAGTCCCAAACACTGTCCTCG 1070 1130 1110 1722 1010 2442 1090 2502 1150 1662 1782 2562 2622 2682 843 863 883 896 g g QQ g рp qq q g ò q ò q δ Q δ g δy g δ ò δ g ò g δ q ò δλ qq δ QQ δλ δ δ ολ à

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82 AGTGAAAGTCCAGGAGTGGGAGTGGGAACGGTGTAATAATGGCTGGAGCATGGAAGCGGT
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 GCAGTCGGGATCCTTGGGGTTGTTCTGTTGGCCATTTTCGTCGCATTATTCTTGACT
                                                      ArgIleSerSerProAlaGluGluThrTrpIleThrCysGluAspArgIleArgValArg
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                                      GlyValValSerLeuAlaProLeuSerLysThrGlySerGlyPheMetTrpValAspAsp
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1141 1181 2741 1221 2801 1261 2921 1281 3041 1341 3221 1393 1101 2441 1121 2501 2561 2621 2681 1201 2861 2981 1301 1321 3101 3161 3281 1161 rCysGluAspArgIleArgValArgGlyGlyAspThrGluCysSerGlyArgValGluIl ||||||::::::::::|||||||::::: |ATGTGACAACAAGATAAGACTTCAGGAAGGACCCACTTCCTGTTCTGGACGTGTGGAGAT CTCATCCCGTCAGTCATCCTTATTGCAGTCGGGATCCTTGGGGTTGTTCTGTTGGCCAT SerGlyPheMetTrpValAspAspIleGlnCysProLysThrHisIleSerIleTrp-Gl | ||| |||| |||::: TGCAGTGAATTGCACAGATATTTCAGTGCAGAAAACCCCCACAAAAAGCCACAACAGGTCG aSerSerGlyHisLeuAlaLeuIleLeuSerSerIlePheGlyLeuLeuLeuLeuValLe AspSerArgCysAlaGlyArgValGluIleTyrHisAspGlyPheTrpGlyThrIleCys GCAGGTCGCTGGCGAGAGTAGAGATCTATCATGAGGGCTCCTGGGGCACCATCTGT GAGATGAAATGCAAAAAGAAATCCCGCATTTGGCAGTGCCATTCACACGGCTGGGGG GlnHisAspCysArgHisLysGluAspAlaGlyValIleCysSerGluPheThrAlaLeu GlyThrTrpGlySerValGlyArgArgAsnIleThrThrAlaIleAlaGlyIleValCys ArgGlnLeuGlyCysGlyGluAsnGlyValValSerLeuAlaProLeuSerLysThrGly eLeuTrpAspCysHisAlaLysProTrpGlyGlnGerAspCysGlyHisLysGluAspAl aGlyValArgCysSerGlyGlnSerLeuLys-------SerLeuAsnAl AspLeuAsnCysThrGlyThrGluSerHisLeuTrpGlnCysProSerArgGlyTrpGly 3102 1375 2202 1042 2262 2322 1.082 2382 1102 2442 2502 1142 2562 1162 2622 2682 1202 2742 2802 1241 2862 2922 1281 2982 1301 3042 1321 3162 1355 3222 1062 1122 1182 1221 1261 1341 pp g qq g q pp Dp g q g Q g ö. ρp q οy g ò q ò ò ογ Qγ δy δ δ δ δ οy δ οy οy ò à

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TGKNWOWGGLSCDNFBEAKVTCSGHREPRLYGGEIPCSGRVEVKHGDWGSVCDFDLSL
EARSVYCRELQCGTVVSILGGAHFGBESGQIWGEEFQCSGDESHLSLCSVAPPLDRTC
THSRDYSVVCSRYIDITLAGGESSCERVELKTLGANGPLCSSHWDMEDAHVLCQQLK
CGVAQSIPEGAHFGKGAGQVWSHMFHCTGTEEHIGDCLMTALGAPTCSEGQVASVICS
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PKWTSESHHGTGHPTLTALLVCGAILLVLLIVFLLWTLKRRRIQRLTVSSRGEVLIHQ
VQYQEMDSRADDLDLKSSGVIQRHTEKENDNL"
85. 198
3220. 3288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="FAT; member of the scavenger receptor cysteine rich
type B superfamily; transmembrane protein type I"
/codon_start=1
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/db_xref="GI:13236131"
/translation="MGGHRWVLLGGAGSPGCKRFVHLGFFVVAVSSLLSASAVTNAPG
                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4402)
Schaer, D.J.; Boretti, F.S., Hongegger, A., Poehler, D., Linnscheid, P., Staege, H., Muller, C., Schoedon, G. and Schaffner, A.
Molecular cloning and characterization of the mouse CD163
homologue, a highly gluccorticoid-inducible member of the
Immunogenetics 53 (2), 170-177 (2001)
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ANSSAGSGYIWMDKVSCTGNESALWDCKHDGWGKHNCTHEKDAGVTCSDGSNLEMRLV
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PHLDDLAGKONBESALWDCKHRGWGKHWCDHABDVGVTCLEGADLSLRLVDGVSRCSG
RLEVRROGEWGTVCDNWDLADASVVCKOLGCPTAISAIGRVASSEGSGOIWLDNISC
EGHBATLWECKHQEWGKHYCHHREDAGVTCSDGADLELRLVGGGSRCAGIVEVELOKL
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                                                                          3392
 3332
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Mus musculus macrophage hemoglobin scavenger receptor CD163
Precursor, mRNA, complete cds.
 --CT
                                       uArgValSerThrArgArgArgGlySerLeuGluGluAsnLeuPheHisGluMetGluTh
                                                                        TGCAGTTTCCTCAAGAGGAGAACTTAGTCCACCAAATTCAATACCGGGAGATGAATTC
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85. .3450
 3282 TTTCGTCGCATTATTCTTGACTAAAAAGCGAAGACAGAGACAGCGG-
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Schaer, D.J., Boretti, F.S. and Schaffner, A.
Direct Submission
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/db_xref="taxon:10090"
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3393 TTGCCTGAATGCAGATGAT 3411
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332
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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οy	617	< €	
g	979	:::	
ر م	637	AsnalaserthrGlyTyrGlyLysIleTrpLeuAspAspValSerCysAspGlyAspGlu 656 	
ογ	657	31u 676	
Dp	1099	GCAACTCTTTGGGAGTGTAAACACCAAGAGGGGAAAGCATTACTGTCATCAT	
oy Oy	677 1159	AspvalGlyvalIleCysSerAspAlaSerAspMetGluLeuArgLeuValGlyGlySer 696                        GACCTGGTGTGACATGTTCTGATGGAGCAGATCTGGAACTTGTAGGTGGAGGC 1218	
٥y	σ	SerArgCysAlaGlyLysValGluValAsnValGlnGlyAlaValGlyIleLeuCysAla 716	
ි සි	1219	AGTCGCTGTGCTGGCATTGTGGAGGTGGAGATTCAGAAGCTGACTGGGAAGATGTGTAG	
ç d	717	AsnGlyTrpGlyMetAsnIleAlaGluValValCysArgGlu 	
ò	737	IleArqValSerArqGluProHisPheThrGluArqThrLeuHisIleLeuWetSerAsn 756	
· 8	1339	CITCAAACCCAGGCIAAGAICTACTCTAAAACTGGGGCAACAAATACGTGGCTCTTTCCT 13	
ογ	757	SerGlyCysThrGlyGlyGluA	
qq	1399	GGATCTTGTAATGGAAATGAAACTACTTTTGGCAATGCAAAA	
ογ	777	ThralacysHisLeuAsnMetGluAlaSerLeuIleCysSerAlaHisArgGluProArg 796	
QQ	1459	CITICCIGIGATAATITCGAAGAAGCCAAAGTIACCTGCTCAGGCCACAGGGAACCCAG	
οy	797	LeuValGlyAlaAspMetProCysSerGlyArgValGluValLySHisAlaAspThr	
qq	1519	CIGGITIGEN	
δ	∺	Args 	
a	1579	GGCTCCGTCTGTGTTTTGACTTGTCTCTGGAAGCTGCCAGTGTGGTGTGCAGGGAATT	
ογ	837	AsnCysGlyAspAlaIleSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeu 856	
д	1639	CANTGIGGAACAGICGICITIATCCIAGGGGGAGCACAITITIGGAGAAGGAAGIGGA	
οy	857	ThrTrpAlaGluLySPheGlnCySGluGlySerGluThrHisLeuAlaLeuCySProIl-	
QD	1699	ATCTGGGGTGAAGAATTCCAGTGTAGTGGGGATGAGTCCCATCTTTCACTATGC	
5 5	877	ValGlnHisProGluAspThrCysIleHisSerArgGluValGlyValValCysSerArg 89	
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g 8	1 6	ACACTCGGAGCCTGGGGTCCCCTCTGCAGTTCTCATTGGGCACATGGAAGATGCTCATGTC 19	
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δ	in	GluargSerValArgValTrpGlyHiSArgPheHiSCySLeuGlyAsnGluSerLeuLeu 976	
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2835 1273 1313 3075 1074 2355 2415 2535 2595 2775 ---AlaGluGluThrTrpIleThrCysGluAspArgIleArgValArgGlyGlyAspThr 1253 2955 3015 1333 3135 1195 AlaProLeuSerLysThrGlySerGlyPheMetTrpValAspAspIleGlnCysProLys 1214 1234 SerTrpAspLeuAlaGluAlaGluValValCysGlnGlnLeuGlyCysGlySerAlaLeu 1293 ValIleCysThrGlySerLeuThrGlnProLeuPheProCys-----LeuAlaAsnVal 1014 SerAspProTyrLeuSerAlaValProGluGlySerAlaLeuIleCysLeuGluAspLys 1034 1094 CysProSerArgGlyTrpGlyGlnHisAspCysArgHisLysGluAspAlaGlyValIle 1134 CysSerGluPheThrAlaLeuArgLeuTyrSerGluThrGluThrGluSerCysAlaGly 1154 1175 AlaIleAlaGlyIleValCysArgGlnLeuGlyCysGlyGluAsnGlyValValSerLeu 1194 1334 AspCysGlyHisLysGluAspAlaGlyValArgCysSerGlyGlnSerLeuLysSerLeu 1353 966 GlyPheTrpGlyThrIleCysAspAspGlyTrpAspLeuSerAspAlaHisValValCys GluCysSerGlyArgValGluIleTrpHisAlaGlySerTrpGlyThrValCysAspAsp AlaAlaLeuArgAspAlaSerPheGlyGlnGlyThrGlyThrIleTrpLeuAspAspMet 2896 GACTGTTCTGGACGTGTGGAGATCTGGCACAAAGGTTCCTGGGGAACAGTGTGTGATGAC 977 AspAsnCysGlnMetThrValLeuGlyAlaProProCysIleHisGlyAsnThrValSer GGAGATTGCCTCATGACTGCTCTGGGTGCGCCGACGTGTTCCGAAGGACAGGTGGCCTCT 1135 ( 1294 1015 1055 2296 1115 2656 1235 2956 3016 3076 2059 2119 2179 1035 2236 1254 1314 1274 997 qq : qq qq qq δý qq ò ò QQ δλ qq g ò qq Ω qq ŏ q B δ qq ò QQ δ qq δ QQ Qγ QQ οy Q δ ò ò g Ω

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PGGTCHHSGSAQVVCSAYSEVRLMTNGSSQCEGQVEMNISGQWRALCASHWSLANANV
ICRQLGCGVAISTPGGPHLVVEEGDQILTARFHCSGAESFLWSCPVTALGGPDCSHGNT
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DQGSWGTICDDGWDLDDARVVCRQLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 4475)
Wijngaard, P.L., MacHugh, N.D., Metzelaar, M.J., Romberg, S.,
Wijngaard, A., Pepin, L., Davis, W.C. and Clevers, H.C.
Members of the novel WCl gene family are differentially expressed
on subsets of bovine CD4-CD8- gamma delta T lymphocytes
J. Immunol. 152 (7), 3476-3482 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                             3310 ------CTTACAGTTTCCTCAAGAGGAGAGGTCTTGATACATCAAGTTCAGTACCAA 3360
                                                                                                                                                                                                                                                1390 HisLeuProLeuArgValSerThrArgArgArgGlySerLeuGluGluAsnLeuPheHis 1409
                                                                                                                                                       -----ArgValGlnLysGlnLys 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-JAN-1992) P.L.J. Wijngaard, Dept of Immunology,
University Hospital, P O Box 85500, 3508 GA Utrecht, THE
AsnAlaSerSerGlyHisLeuAlaLeuIleLeuSerSerIlePheGlyLeuLeuLeu
                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein_id="CAA45255.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="WC1.1 subcluster
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                                                                                                                                                    1374 ValLeuPhelleLeuPheLeuThrTrpCys----
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1. .4475
/organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_line="D409/N2"
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/product="BoWC1.1"
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/isolate="D409"
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Wijngaard, P.L.J.
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KQLGCGEALDATVSSFFGTGSGPIWLDEVNCRGEESQVWRCPSWGWRQHNCNHQEDAG
VICSGFVRLAGGDGPCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAELGCGKAVSVLG
HWPFRESDGQVWAEEFRCDGGEPELWSCPRVPCPGGTCLHSGAAQVVCSVYTEVQLMK
                                                                                                                                                                                                                  LAEAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAEEVPVPGTPSPSQGNEEEVPPE
KEDGVRSSQTGSFLNFSREAANPGEGEESFWLLQGKKGDAGYDDVELSALGTSPVTFS
                                                                                          SAASEESSPYCSDSRQLRLVDGGGPCGGRVEILDQGSWGTICDDDWDLDDARVVCRQL
GCGEALNATGSAHFGAGSGPIWLDDLNCTGKESHVWRCPSRGWGRHDCRHKEDAGVIC
                                                                                                                              SEFLALRAVSEDQQCAGWLEVFYNGTWGSVCRSPWEDITVSVICRQLGCGDSGSLNTS
VGLREGSRPRWYDLIQCRKMDTSLWQCPSGPWKYSSCSPKEEAYISCEGRRPKSCPTA
                                                                                                                                                                                  VRSAAFGPGNGSIWLDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLP
                                                      NGTSQCEGQVEMKISGRWRALCASHWSLANANVVCRQLGCGVAISTPRGPHLVEGGDQ
                                                                       ISTAQFHCSGAESFLWSCPVTALGGPDCSHGNTASVICSGNHTQVLPQCNDFLSQPAG
                                                                                                                                                                AACTDREKLRLRGGDSECSGRVEVWHNGSWGTVCDDSWSLAEAEVVCQQLGCGQALEA
                                                                                                                                                                                                   TTTAGTRTTSNSLPG1FSLPGVLCL1LGSLLFLVLV1LVTQLLRWRAERRALSSYEDA
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222 IleLeuCysGlnGlyAsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTrpGlyAsn 241

q	622	:::
ò	242	erAspLe
q	682	CACACAGTGGATCTGCTCAGGTTGTTTG
Qy	262	LeuargLeuValGlyGlyThrasnargCysMetGlyArgValGluLeuLysILeGlnGly 281     :::
Qy Dp	282 799	ArgtrpGlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaAspValValCysLys 301 
λ̈́o	0	euGlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGlnSerGlySer 32
q	859	
oy Op	322	AspvalvaltrpLeuAspGlyValSerCysSerGlyAsnGluSerPheLeuTrpAspCys 341
δý	342	ArgHisSerGlyThrValAsnPheAspCysLeuHisGlnAsnAspValSerValIleCys 361
g	979	CCTGTGACTGCCCTGGGTCCTGACTGTTCCCATGGCAACACAGCCTCTGTGTATCTGC 1038
ογ	362	SerAspGlyAlaAspLeuGluLeuArgLeuAlaAspGlySerAsnAsnCysSerGlyArg 381
QQ	1039	AAAC
ολ	382	ValGluValArgIleHisGluGlnTrpTrpThrIleCysAspGlnAsnTrpLysAsnGlu 401
q	1048	
ογ	402	CysProPheSerValP
g	1069	
ογ	422	AlaLysProSerAsnGluAlaArgAspIleTrpIleAsnSerIleSerCysThrGlyAsn 441
qq	1084	TCTCAACCTACAGGCTCTGCGGCCTCA1110
οý	442	GluSerAlaLeuTrpAspCysThrTyrAspGlyLysAlaLysArgThrCysPheArgArg 461
QQ	1110	1110
λο a	462	111eCysSerAspLysAlaAspLeuAspLeuArgLeuValGlyAla 48
g	1111	
φ 6	482	HisSerProCysTyrGlyArgLeuGluValLysTyrGlnGlyGluTrpGlyThrValCys 501
γ	20	isaspargTrpSerThrargasnalaalavalValCysLysGlnLeuGlyCysGlyLys 52
QQ	1225	
λ̈́o	522	ProMetHisValPheGlyMetThrTyrPheLysGluAlaSerGlyProlleTrpLeuAsp 541
qq	1285	GCCCTCAATGCCACGGGTCTGCTCACTTCGGGCCAGGATCAGGGCCCATCTGGTTGGAC 1344
. රු යු	542	AspvalSercysileGlyAsnGluSerAsnIleTrpAspCysGluHisSerGlyTrpGly 561 ::::::::
ò	562	LysHisAsnCysValHisArqGluAspValIleValThrCysSerGlyAspAlaThrTrp 581
g 2	1405	GAGTTCCTG 14
ογ	582	GlyLeuArgLeuValGlyGlySerAsnArgCysSerGlyArgLeuGluValTyrPheGln 601

1459 GCCCTCAGGATGGTGAGTGAGGACCAGCAGTGTGCTGGGTGGCTGGAAGTTTTCTACAAT 1518 1519 GGGACCTGGGGCAGTGTCTGCCGTAACCCCATGGAAGACATCACTGTGTCCACGATCTGC 1578 861 CGCTGGGACCTGGACCCCGTGTGGCTGCCAAGCAGCTGGGCTGTGGAAGCCCTG 1920 ||| ||| ||| :::||||:::||| |155 CCAGTGTCTGATGGAAACTTCACACTGCCCAGTGCAGTCATCTGTGCAGAGCTGGGA 2214 2335 CCCTGTCCAGGAGGCACATGTCTCCACAGGGGGGCTGCTCAGGTTGTCTGTTCAGTGTAC 2394 ::: ||| ||| :::|||||| ||| ALCTCTGGACGCCCAATGTT 2514 SerGlnLeuAspCysProSerSerIleIleGlyMetGlyLeuGlyAsnAlaSerThr--- 640 698 ArgCysAlaGlyLysValGluValAsnValGlnGlyAlaValGlyIleLeuCysAlaAsn 717 818 SerValCysAspSerAspPheSerLeuHisAlaAlaAsanValLeuCysArgGluLeuAsn 837 ThraspvalargLeuval---AsnGlyLysSerGlnCysAspGlyGlnValGluIleAsn 916 658 AspLeuTrpSerCysArgAsnSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAsp 677 678 ValGlyValIleCysSerAspAlaSerAspMetGluLeuArgLeuValGlyGlySerSer 697 738 ArgValSerArgGluProHisPheThrGluArgThrLeuHisIleLeuMetSerAsnSer 757 758 GlyCysThrGlyGlyGluAlaSerLeuTrpAspCysIleArgTrpGluTrpLysGlnThr 777 778 AlaCysHisLeuAsnMetGluAlaSerLeuIleCysSerAlaHisArgGlnProArgLeu 797 798 ValGlyAlaAspMetProCysSerGlyArgValGluValLySHisAlaAspThrTrpArg 817 CysGlyAspAlaIleSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThr 857 GlnHisProGluAspThrCysIleHisSerArgGluValGlyValValCysSerArgTyr 897 GlyArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaAlValCys ValLeuGlyHisTrpGlySerLeuCysAspThrHisTrpAspProGluAspAlaArgVal ------GlyTyrGlyLysIleTrpLeuAspAspValSerCysAspGlyAspGluSer 838 2455 602 622 2395 878 641 qa : QQ QQ qq g QQ OD q ò δ QQ οy qq g δ δ g δ qq δy δy q οy ŏ δ Ωý Qγ δy Ω οy ò ò

u 976     2634	r 996 I 2694	p 1016 A 2754	u 1036     2814	ue 1056 C 2874	s 1076 : G 2934	y 1096   G 2994	o 1116   T 3054	r 1136 	u 1156 	e 1176 T 3228	o 1196 T 3288	s 1216 T 3348	u 1236     3408	- 1243 C 3468	u 1260     3528	a 1280 	r 1300 : 3648
ValargValTrpGlyHisArgPheHisCysLeuGlyAsnGluSerLeuLe: :::::: GATCAGATCTCAACAGCCCAATTTCACTGCTCAGGGGTGAGTCCTTCCT	sGlnMetThrValLeuGlyAlaProProCysIleHisGlyAsnThrValSer   :::	SThrGlySerLeuThrGlnProLeuPheProCysLeuAlaAsnValSerAsp  :::   ::	erAlaValProGluGlySerAlaLe        TGCGCCTCAGAGGAGATTCTCC	saspGlyPh     ccaGGGCTC	TrpGlyThrIleCysAspAspGlyTrpAspLeuSerAspAlaHisValValCysGlnLys 	GlyValalaPheasnalaThrValSeralaHisPheGlyGluGlySerGly 	.leuAspAspLeuAsnCysThrGlyThrGluSerHisLeuTrpGlnCysPr. 	GlyTrpGlyGlnHisAspCysArgHisLysGluAspAlaGlyValIleCysSe  	AlaLeuArgLeuTyrSerGluThrGluThrGluSerCysAlaGlyArgLeu 	luvalPheTyrAsnGlyThrTrpGlySerValGlyArgArgAsnIleThrThrAlail( 	eValCysArgGInLeuGlyCysGlyGluAsnGlyValValSerLeuAlaPr. ::::	sThrGlySerGlyPheMetTrpValaspaspIleGlnCysProLysThrHis 	riletrpGinCysLeuSerAlaProTrpGiuArgArgileSerSerProAlaGl  :::	hrtrpilethrcysglu	Aspargileargvalargglyglyaspthrglucysserglyargvalgl 	rpHisAlaGlySerTrpGlyThrValCysAspAspAspSerTrpAspLeuAlaGluAl. 	GluValValCysGlnGlnLeuGlyCysGlySerAlaLeuAlaAlaLeuArgAspAlaSer 
GluArgSerVal      GAAGGAGGTGAT	AspAsnCys :::    TGGAGTTGT	ValileCys	ProTyrLeuS       CCTGCAGGCT	ArgLeuVal             CGCCTGGTG	TrpGlyThr          TGGGGCACC	LeuGlyCys(           CTGGGCTGT(	ProlleTrpI               CCCATCTGGC	SerArgGly            TCCGGGGG	GluPheThr?          GAGTTCCTGG	GluValPhe 	AlaGlyIle ::: GrGrccGr	LeuSerLys'::: GGTCTCAGG	11eSerIle     ::: ACCTCTCTC	GluThrTrp      GAAGCCTAC	ACAGACAGA	IleTrpHis:::	GluValVa 
957	977	997	1017 2755	1037 2815	1057 2875	1077 2935	1097	1117 3055	1137 3115	1157 3169	3229	1197 3289	1217 3349	1237 3409	1244	1261	1281
Qy Dp	Qy Dp	Qy Db	9. 9.	Qy Dp	Qy Db	Qy Db	OY Db	OY Db	Oy Db	Qy Db	QY Db	QY Db	Oy Dp	Qy Dp	Oy Dp	Q.y	QY dg

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Manmalia; Butheria; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 7656)

Mollenhauer. J., Holmskov, U., Wiemann, S., Krebs, I., Herbertz, S., Madsen, J., Kioschis, P., Coy, J.F. and Poustka, A.

The genomic structure of the DMBTI gene: evidence for a region with susceptibility to genomic instability

20065089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens mRNA for DMBT1 protein 8kb transcript variant 1 (DMBT1/8kb.1).
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Submitted (18-JUN-1999) Mollenhauer J., Molecular Genome Analysis,
Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, 69120
Heidelberg, GERMANY
3945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3769 GCTGGTGTGAGGTGCTCTGGTGTAAGGACAACATTGCCCACGACCACGACAGGGGACCAGA 3828
                                                                                                                                                                                                                                         1348 ------GlnSerLeuLysSerLeuAsnAlaSerSerGlyHisLeuAlaLeuIleLeu 1364
                                                                                                                                                                                                                                                                                                                                                                                                1385 ValGlnLysGlnLysHisLeuProLeuArgValSerThrArgArgArgGlySerLeuGlu 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                        3946 GCAGAGCGC-------AGAGCCTTATCCAGCTATGAAGATGCTTTGCT 3987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1405 GluAsnLeuPheHisGluMetGluThrCysLeuLysArgGluAspProHisGlyThrArg 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1425 ThrSer---AspAspThrProAsnHisGlyCysGluAspAlaSerAspThrSerLeuLeu 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4048 GAICAGAIGACIGAIGICCCTGAIGAAAATTAIGAIGAIGAIGAAGAAGIACCAGIGCCT 4107
                                                                                                                                                                                                                                                                                                                     1365 SerSerIlePheGlyLeuLeuLeuValLeuPheIleLeuPheLeuThrTrpCysArg 1384
                                                                                                                                                                                                                                                             3829 ACAACCICAAATICTCICCCIGGCATCTCICCCIGCCIGGGGTTCTCTGTGTTATCCIG
                                                                                                                                                                                                                                                                                                                                            3889 GGGTCGCTTCTTCTGGTCCTGGTCACTGGTGACTCACTACTCAGATGG---AGA
                                                                                                                                                              1341 AlaGlyValArgCysSerGly-----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4108 GGAACTCCTTCTCCCTCTCAGGGGAATGAG 4137
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1.7656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ243224
AJ243224.1 GI:6624921
DMBT1 gene; DMBT1/8kb.1 protein.
human.
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/map-"10425.1"
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1. 7318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
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Mollenhauer, J.
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VERSION
KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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MEDLINE
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HSA243224
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PTBSPDTWPTSHASTAGSESSLALRLYNGGDRCOGRVEVLYRGSWGTVCDDYWDTNDA
NVVCRQLGCGWAMSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHDGWLSHNCGHH
EDAGVICSASQSQPTPSPDTWPTSHASTAGSESSLALRLYNGGDRCQGRVEVLYRGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTVCDDYWDTNDANYVCROLGCGWATSAPGRARFGGGSGPIYLDDVRCSGHESYLWSC
PHNGWLSHNCGHHEDAGVICSASQSQPTPSPDTWPTSHASTAGSESSLALRLVNGGDR
CQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWATSAPGSARFGGGSGPIALDD
                                                                                                                                                                                                                                                                                                                                                                                                                                  AEGSPFPSELTLESTAAEGSPISLESTLEŠTVAEGSLIPSESTLESTVAEGSDSGLAL
RLVNGDGRCQGRVELLYRGSWGTVCDDSWDTNDANVVCRQLGCGWAMSAPGNAWFGQG
SGPIALDDVRCSGHESYLWSCPHNGWLSHNCGHGEDAGVICSAAQPQSTLRPESWPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPPVPTEGSESSLALRLVNGGDRCRCRVEVLYRGSWGTVCDDYWDTNDANVVCRQLG
CGWAMSAPGNAQFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLTHNCGHSEDAGVICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDDSWDTNDANVVCRQLGCGWAMLAPGNARFGQGSGPIVLDDVRCSGNESYLWSCPHN
GWLSHNCGHSEDAGVICSGPESSLALGLVNGGDRCQGRVEVLYRGSWGTVCDDSWDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DANVYCRQLGCGWATSAPGNARFGQGSGPIVLDDYRCSGHESYLWSCPNNGWLSHNCG
HHEDAGVICSAAQSRSTPRPDTLSTITLPPSTVGSESSLTLRLVNGSDRCQGRVEVLY
RGSWGTVCDDSWDTNDANVYCRQLGGGWATSAPGNARFGQGSGPIVLDDVRCSGHESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGDRCQGRVEVLXRGSWGTVCDDSWDTSDANVVCRRLGCGWATSAPGNARFGQGSGPI
VLDVRCGSYESYLWSCPHVOMLSHVOOJSEDAGVICSAAHWSTPSPDTLPTTTLPA
STVGSESSLALRLWGGDRCQGRVEVLYGGSWGTVCDDSWDTNDANVVCRQLGCGWAM
SAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHSEDAGVICSASQSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASOSOPTPSPDTWPTSRASTAGSE
STALALLVWOGDRCRRCRVEVLYGSWORTVCDDYWDTNDANVCRQLGGCGWAMSABGNA
OFGGGSGFTVLDDWRCSGHESYLMSCPHNGWLSHNCGHHEDAGVICSAAQSGSTPRPD
TWLTTNLPALTVGSESSLALRLVNGGDRCRGRVEVLYRGSWGTVCDSWDTNDANVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQLGCGWAMSAPGNARFGQGSGPIVLDDVRCSGNESYIWSCPHKGWLTHNCGHHEDAG
VICSATQINSTTTDWWHPTTTTTARPSSNCGGFLFYASGTFSSPSYPAYYPNNAKCVW
EIEVNSGYRINLGFSNLKLEAHHNCSFDYVEIFDGSLNSSLLLGKICNDTRQIFTSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLGFSASDLVISTWNGYYECRPQITPNLVIFTIPYSGCGTFKQADNDTIDYSNFLTAA
VSGGIIKRRTDLRIHVSCRMLQNTWVDTMYIANDTIHVANNTIQVEEVQYGNFDVNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISDANVVCRQLGCGWAISAPGNARFGQGSGPIVLDDVRCSGYESYLWSCPHNGWLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWSCPHNGWLSHNCGHHEDAGVICSVSQSRPTPSPDTWPTSHASTAGSESSLALRLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRWITHFRSDISFQNTGFLAWYNSFPSDATLRLVNLNSSYGLCAGRVEIYHGGTWGTV
CDDSWTIQEAEVVCRQLGCGRAVSALGNAYFGSGSGPITLDDVECSGTESTLWQCRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWFSHNCNHREDAGVICSGNHLSTPAPFLNITRPNTDYSCGGFLSQPSGDFSSPFYPG
                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:Q9UGM2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APLSRPTPSPDTWPTSHASTAGPESSLALRLVNGGDRCOGRVEVLYRGSWGTVCDDSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCQHSEDAGVICSDTLPTITLPASTVGSESSLALRLVNGGDRCQGRVEVLYRGSWGTV
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DLIRSGCVRDDTYGPYSSPSLRIARFRRRAFHFLNRFPSVYLRCKMVVCRAYDPSSRC
                                                                                                                                                                         is
                                                                                                                                                                         that
                                                                        tumour suppressor, role in
                                                                                                                                                                            gene
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                                                                                                                                   /note="8kb protein, variant 1
alternative splice form of the DMBT1
expressed in human adult lung"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein"
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Indels:
Gaps:
                                                                                                                                                                                                                                                                   /product="DMBT1/8kb.1 protein"
/protein_id="CAB63942.1"
                                                                                                    system and differentiation"
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2126 c 2166 g 1
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44 ThraspLeuGluLeuArgLeuValasnGlyAspGlyProCysSerGlyThrValGluVal 63

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                                                                                                                                                                                                                                                                            AspGlyAsnAsnSerCysSerGlyArgValGluValLysPheGlnGluArgTrpGlyThr 178
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                                                                           GluSerAlaLeuTrpGluCysGlnHisArgGluTrpGlySerHisAsnCysTyrHisGly 140
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                                                             ValValCysLysGlnLeuGlyCysProPheSerPheAlaMet------PheArgPhe 100
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194 TCCAGTTTGGCCCTGAGGCTGGTGAATGGAGGCGACAGGTGTCGAGGCCGAGTGGAGGTC 853
                  1145 TGGCCGACCTCACATGCATCAACAGCAGGACCTGAATCCAGTTTGGCCCTGAGGCTGGTG
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                                        CTATACCGAGGCTCCTGGGGCACCGTGTGATGACTACTGGGACACCCAATGATGCCAAT
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uGlnAla 403      TGATGCC 1984	Marys 423	snGluSer 443 ::       ATGAGTCC 2104	SerAsp 463     GAAGAT 2164	TGTCG 2224	Jeuval 479	31yThr 499           GCACC 2344	31yCys 519         GCTGT 2404	[letrp 539     NTTGTT 2464	SerGly 559 :::  } \ATGGC 2524	576 rcccag 2584	581 GGTCT 2644	leuGlu 597        STGGAG 2704	Maala 617     	31yAsn 637 3CCCGG 2824	31uSer 657            3AGTCC 2884	Sluasp 677          Saagac 2944	TGCCG 3004
4 ValargileHisGluGlnTrpTrpThrileCysAspGlnAsnTrpLysAsnGl 	404 LeuValValCysLysGlnLeuGlyCysProPheSerValPheGlySerArgArgAlaLy 	4 ProSerAsnGluAlaArgAspIleTrpIleAsnSerIleSerCysThrGlyA	4 AlaLeuTrpAspCysThrTyrAspGlyLysAlaLysArgThrCysPheArgArg 	464 AlaGlyvalIleCysSer	0	480 GlyAlaHisSerProCysTyrGlyArgLeuGluValLysTyrGlnGlyGluTrpGlyThr 	500 ValcysHisaspargTrpSerThrArgAsnalaalaValValCysLysGlnLeuGlyCys 	520 GlyLysProMetHisValPheGlyMetThrTyrPheLysGluAlaSerGlyProIleTrp 	0 LeuaspaspValSerCysIleGlyAsnGluSerasnIleTrpaspCysGluHisSerGly	560 TrpGlyLySHiSASnCySValHiSArgGluAspVallleValThrCySSer	577	2GlyLeuArgLeuValGlyGlySerAsnArgCysSerGlyArgLeuGlu 	8 ValtyrPheGlnGlyArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAla	8 AlaValValCysSerGlnLeuAspCysProSerSerIleIleGlyMetGlyLeuGlyAsn	8 AlaSerThrGlyTyrGlyLysIleTrpLeuAspAspValSerCysAspGlyAspGluSer	58 AspLeuTrpSerCysArgAsnSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAsp 	8 ValGlyValIleCysSerAspAla
Qy 38. Db 192	Qy. 40.	Qy 42.	Oy 44-	Oy 46. Db 216	Qy 47	Oy 48	Qy 50 Db 234	Qy 52 Db 240	Qy 54 Db 246	Qy 56 Db 252	Qy 57 Db 258	Qy 58 Db 264	Qy 598 Db 2705	Qy 61 Db 276	Qy 63 Db 282	Qy 65 Db 288	Oy 67 Db 294

Οy	989	SerAspMetGluLeuArgLeuVal	693
QQ	3005 ACCATCACCTTGCCTGCATCGAC	ccagrirgecccreagecreer	
Qγ	694 GlyGlySerSerArgCysAlaGly	gcysAlaGlyLysValGluValAsnValGlnGlyAlaValGlyIle	713
qq	3065 AATGGAGGTGACAG	CTGGGGCA	
Qy	71	AsnileAlaGluValValCysArgGlnLeuGluCys	33
QQ	3125 GTGTGCGATGA	2aatgatgccaatgtcgtctgcaggcaactgggctgt	-
δλ	734 GlySerAlail	eArgValSerArgGluProHisPheThrGluArgThrLeuHisIleLeu	53
Q Q	3185 GGCTGGGCCAT	CATTGE	3244
Oy .	754 MetSerAsnSerG	luAlaSerLeuTrpAspCysIleArgTrpGl   :::	73
qq	3245 CTGGATGATGTGCGCTGC	AGTCTTACCTGTGGAGCTGCCCCCACAT	3304
δŏ	774 TrpLysG	inMetGluAlaSerLeuIleCysSerAlaH	93
QQ	3305 TGGCTCTCCCACACTGTGG	ilgaagacerigiterretecreaetreeea	3364
Оу	794GlnPro		95
qq O	3365 TCCCGGCCAACACCTAG	CACTIGGCCAACCICACAIGCAICAACAGCAGGAICI	3424
δλ	1967	-ArgLeuValGlyAlaAspMetProCysSerGlyArgValGlu	0
QQ	3425 GAATCCAGTTTGGCCCT	srercaeeecceaere	3484
δy	810 ValLysHisAlaAspThrTrpArgSe	JSerValCysAspSerAspPheSerLeuHisAlaAla	829
QQ	3485 GTC	CCTGTGTGTGACTACTGGGACACCAATGA	3544
QY	830 AsnvalLeuCysArgGluLeuAsnCysGlyAspAlaIl	CysGlyAspAlaIleSerLeuSerValGlyAspHis	849
qa .	3545	STCAGCCCCAGGAAATGC	3604
Qy	850	cTrpAlaGluLysPheGlnCysGluGlySerGluThr	698
QQ	3605 T	SCTCAGGACATGA	3664
Qy	870	ysIleHisSerArgGl	889
Op	3665 T	STGGCCATCATGAAG	3724
Qy	v 068	rhrasp	899
qq	3725 G	CCAGTCCCAGCCGACACCCAGCCCAGACACTTGGCCA	3784
δλ	006	ValArgLeuValAsnGly	905
qq	3785 ACC	TCTGAATCCAGTTTGGCCCTGAGGCTGGTGAATGG	8
Qy	906 LysserGlnCysAspGl)	GInValGluIleAsnValLeuGlyHisTrpGlySerLeuCys	925
qq	3845 GGTGACAGGTGTCAGGG	CTATACCGAGGCCCCTGGGGCACCGTGTG	6
δλ	926 AspThrHisTrpAspProG	LeuCysArgGlnLeuSerC	945
qq	3905 GATGACTACTGGGACACCA	SCAGGCAGCTGGGCTGTGG	σ
Qy	946 AlaLeuSerThrThrGlyGlyLy	STyrIleGlyGluArgSerValArgValTrpGlyHis	965
, qq	3965 GCCACGTCAGCCCCAGGAAAT	cggtridgccagggtrcaggacccarrgrcrg	4024
Qy	966 ArgPheHisCysLeuGlyAsnGl	uSerLeuLeuAspAsnCysGlnMetThrValLeuGly	985
Dp	4025 GATGTGCGCTGCTCAGG	CCTATCTGTGGAGCTGCC	4084
QY	986 AlaProProCysIleHisGlyAsn1	nThrVaiSerValIleCysThrGlySerLeuThrGln	1005

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::: ||| || || || TCCCACAACTGTGGTGTTCTGCTCATCCAGTTCCCAGTCCCAG 4144
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                                                                                                                  1046 AlaGlyArgValGluIleTyrHisAspGlyPheTrpGlyThrIleCysAspAspGlyTrp 1065
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                                                  4145 CCGACA---CCCAGCCCAGACACTTGGCCAACCTCGCATGCATCAACAGCAGGATCTGAA
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                              ProLeuPheProCysLeuAlaAsnValSerAspProTyrLeuSerAlaValProGluGly
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linear PRI 17-SEP-1999
transcript variant 2
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/note="Sequence is an alternative splice form of the DMBT1 gene that is expressed in human adult trachea. Isoforms of DMBT1 are identical to the collectin binding protein gp-340. Full-length cDNA clone contains 1 bp deletions in codons 100 and 1751, that were corrected by comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGPIALDDVRCSGHESYLMSCPHNGMLSHNCGHGEDAGVICSAAQPQSTLRPESWPVR
ISPYPTEGSESSLALBLYNGGDRCRGRVEVLYRGSWGTVCDDYWDYNDNVVCRQLG
CGWAMSAPGNAGFGGGSGPIYLDDVRCSGHESYLWSCPHNGWLTHNCGHSEDAGVICS
APQSRPTPSPPTPSPTYRGSGPIYLMSCPRESSLALBLYNGGDRC
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AEGSPFPSELTLESTVAEGSPISLESTLETTVAEGSLIPSESTLESTVAEGSDSGLAL
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1 (bases 1 to 7683)
Holmskov,U., Mollenhauer,J., Madsen,J., Vitved,L., Gronlund,J., Tornoe,I., Kliem,A., Reld,K.B., Poustka,A. and Skjodt,K. Cloning of gp-340, a putative opsonin receptor for lung surfactant protein D
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280, 69120
                                                                                                                    5185
                                      GCTGGGCCATGTCGGCCCCAGGAAATGCCCGGTTTGGCCAGGGCTCAGGACCCATTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 96 (19), 10794-10799 (1999)
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Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 28
                                                                                                                                                                                                                                                                                                                  Homo sapiens mRNA for DMBT1 protein 8kb barana, a.72,2,3,2
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/protein_id="CAB56155.1"
/db_xref="G1:5912464"
                                                                                                                                                                                                        1350 LeuLysSerLeuAsnAlaSerSerGlyHis 1359
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ATAAATTCTACTACGACAGATTGGTGGCAT 5335
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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AJ243212.1 GI:5912463
DMBT1 gene; DMBT1/8kb.2 protein.
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/tissue_type="trachea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
1. .7683
/gene="DMBT1"
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/gene="DMBT1"
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/gene="DMBT1"
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Mollenhauer, J.
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                                                                                  1025 GAGTCCTACCTGTGGAGCTGCCCCCACAATGGCTGGCTCACCCACAACTGTGGCCATAGT 1084
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TGGGCCATGTCAGCCCCAGGAAATGCCCGGTTTGGTCAGGGCTCAGGACCCATTGTCCTG
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                                             1085 GAAGACGCIGGIGICATCIGCICAGCICCCAGICCCGGCCGACACCCAGAIACT
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q	2225 CGGTCGACGCCCAGGCCAGACACGTTGTCGACCATCACGTTACCTCCATCGACAGGG	Æ	2284	
à	47	-	489	
g	2285		2344	
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λά	510		529	
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<u>ک</u> ۾	530 TyrPheLysGlualaSerGlyProlleTrpLeuAspAspValSerCysIleGlyAsnGl	ສ <b>–</b> ບ	549 2524	
λa	550		269	
g	2525		2584	
à a	570 AspvalllevalThrCysSer		581 2644	
λo	582GlyLeuArgLeuValGl	>	587	
qq	2645 CCGACCTCACATGCATCAACAGCAGGACCTGAATCCAGCTTG	H	2704	
γα			607	
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ž a	608 CysaspaspGlyTrpasnSerLysalaalaalavalvalCysSerGlnLeuAspCysPro		627 2824	
λ	628 SerSerilelleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyrGlyLysIleTrpLeu		647	
q	2825 TGGGCCACGTCAGCCCCCAGGAAATGCCCCGGTTTG		2884	
λά	648 AspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCysArgAsnSerGlyTrp	_	299	
q	2885		2944	
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g	3005 IGGICGACGCCCAGICCAGACACATIGCCGACCAICACCTIGCCIGCAICGACAGIAGG	∢	3064	
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g	3065		3124	
S G	704 GluvalAsnvalGlnGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGlyMetAsnIle		723	
ò	724		743	
g q	31		ď	

<u>&gt;</u> 4	744	SPheThrGluArgThrLeuHisIleLeuMetSerAsnSerGlyCysThrGlyGlyGlu 76	9 9
ā	74	GGTTTGGTCAGGGTCAGGACCCATTGTCCTGGATGAGGCGCTGCTCAGGACACGAG 33	
<b>≿</b> g	3305	AlaSerLeuTrpAspCysIleArgTrpGluTrpLysGlnThrAlaCysHisLeuAsnMet 78 ::	83 364
ξ, q		CAGACACTIGG 3	95
λ		rgLeuValGly 7	
ą	3425	GGCTGGTGAAT 3	
λ	∞ .	rpArgSerVal 8	-
q	3485	GGGCACCGTG 3	544
ž ą	820 3545	rLeuHisAlaAlaAsnValLeuCysArgGluLeuAsnCysGly 8 :::               ::ACCAATGATGTGGCTTGCAGCAGCTGGGCTGTGGC 3	39
λ	840	AspAlaileSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThrTrpAla 85	59
q	3605	3	664
ζ.	860	GluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCysProlleValGlnHis 87	r
ą	3665	GATGATGTGCGCTGCTCAGGACATGAGTCCTATCTGTGGAGCTGCCCCCCACAATGGCTGG 37	7
λ	880	œ	66
q	3725	3	784
λγ	899	68	66
q.	3785	m	844
λy	006	ValArgLeuValAsnGlyLysSerGlnCysAspGlyGlnValGluIle 91	15
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<u>۲</u> و	916	16 ASnValLeuGlyHiSTrpGlySerLeuCySASpThrHiSTrpASpProGluAspAlaArg 93	35 964
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	956	3luArgSerValArgValTrpGlyHisArgPheH	7
ą		GCTGCTCAGGACATGAGTCCTAT 4	0
λ	916	roCysIleHis	6
ą	4085	FIGGAGCTGCCCCACAATGGCTGGCTCTCCCACAACTGTGGCCATCATGAAGACGCT 4	144
ζ	966	ySerLeuThrGlnProLeuPheProCysLeuAlaAsnValSer 1	0
q	4145	ATCTGCTCAGCTTCCCAGTCCCAGCCGACACCCAGCCCAG	201
<u></u>	1016	aLeuIleCysLeuGluAspLysArg 1	035
ą	4202	Argcaicaacagcaggarctgaarccagtitg	243
<u>۲</u> ۲	1036	LeuargLeuvalaspGlyaspSerargCysalaGlyargValGlulleTyrHisaspGly 10              :::::    -           ::::::    -	303
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HSAZY/935 7667 bp mRNA linear PRI 12-JAN-2002
HOMO Sapiens mRNA for DMBT1 8 kb transcript variant 2 (DMBT1 gene).
AJ297935
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AEGSPFPSESTLESTVAEGSPISLESTLESTVAEGSLIPSESTLESTVAEGSDSGLAL
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RVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCSWATSAPGNARFGQGSGPIVLDDVRC
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n Neuenheimer Feld 280, 69120
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Anotes "Dangal Bkb transcript variant 2
deleted in malignant brain tumors 1
alternative splice variant, contains all exons except for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGPIALDDVRCSGHESYLWSCPHNGWLSHNCGHGEDAGVICSAAQPQSTLRPESWPVF
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                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    AJ297935.1 GI:14715230 alternative splicing; deleted in malignant brain tumors 1; DMBT1 gene; DMBT1/8kb.2 protein.
                                                                                                                                                                                                                                                                                                                     Mollenhauer, J., Herbertz, S., Helmke, B., Kollender, G., Krebs, I., Madsen, J., Holmskov, G., Sorger, K., Schmitt, L., Wiemann, S., Otto, H.F., Grone, H.J. and Poustka, A.
Deleted in Malignant Brain Tumors 1 is a versatile mucin-like molecule likely to play a differential role in digestive tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="putative role in mucosal protection, immune
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/tissue_type="small intestine"
/dev.stage="adult"
88. .7329
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/product="DMBT1/8kb.2 protein"
/protein_id="CAC44122.1"
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Submitted (09-NOV-2000) Mollenhauer J
Deutsches Krebsforschungszentrum, Im
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/db_xref="taxon:9606"
/chromosome="10"
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1. .7667
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/gene="DMBT1"
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Mollenhauer, J.
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SGHESYLWSCPHNGWFSHNCGHHEDAGVICSASQSQPTPSPDTWPTSHASTAGSESSL

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TSRASTAGSESTLALRLYNGGDRCRGRVEVLYGGSWGTYCDDYWDDNAVYCRQLGGGWAMSAPGGRAQFGGSGPTYLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGYICSAGAGSGPTYLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGYICSAGOSTPRPDTWLTTTLALFUYGSSSLALRLLWGGDRCRGRYEVLYRGSWGTYCDDSWDTNDANVYCRQLGAMAAPGNRRFGGSGSPTYLDDVRCSGNESYLWSCPHKGWLTHNCGHHEDAGVICSATQINSTTTDWWHPTTTTTARPSSNCGGFLFYASGTFSSSPSYPA
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IDYSNFLTAAVSGGIIKRRTDLRIHVSCRMLQNTWVDTMYIANDTIHVANNTIQVEEV
                                                                                                                                                                                                                                      QYGNFDVNISFYTSSSFLYPVTSRPYYVDLNQDLYVQAEILHSDAVLTLFVDTCVASP
YSNDFTSLTYDLIRSGCVRDDTYGPYSSPSLRIARFRFRAFHFLNRFPSVYLRCKMVV
ALRLVNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWATSAPGNARFG
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163. .7326
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Best Local Similarity:
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                                                                                          TrpGlyAsnHisAspCysSerHisAsnGluAspValThrLeuThrCysTyr-----
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6 GCCAATGTGGTCTGCAGGCAGCTGGGCTGGGCCCCCGGGCACATGCC 0 TyrPheLysGlualaSerGlyProlleTrpLeuAspAspValSerCysIleGlyAsnGlu	CCGACCTCACATCAACAGGATCTGAATCCAGTTGCCCTGAGGTTGTGTGTG	CysAspAspGlyTrpAsnSerLysAlaAlaAlaValValCysSerGlnLeuAspCysPr 	a spraisticysabolyspoilyspecingly and spraisticys and spraisticy and spraistic and spr	TGGTCGACGCCCAGTCCAGACATTGCCGACCATCACCTTGCCTGCATCGACAGTAGGSerAspNetGluLeuArgLeuValGlyGlySerSerArgCysAlaGlyLysVa	AlaGluValValCysArgGlnLeuGluCysGlySerAlaIleArgValSerArgGlu [	
2386 530 2446 550 2506 570 2566	58 58 58	608 2746 628 2806 648	2866 2866 668 2926 685	0 0 4 0 0	724 3166 744 3226 764 3286	784 3346 796 3406 800
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4587	HOAGCHHCCCAGHCCCAGHCGACACCCAACHCAACACAACHHGGCCAACCHCGHCCAACA	4525	4
113		1135	δŏ
1139	ProSerArgGlyTrpGlyGlnHisAspCysArgHi 	1116	OY Db
446	GIYTOILEIT PLEUASPASPLEUASICYSIILE             GGACCCATTGTCCTGGATGATGTGCGCTGCTCAG	4405	op Op
	CAGCTGGGCTGGGCTGGGCCACGTCAGCCCCAGGAATGCCCGGGTTTGGCCAGGGTTC		an .
109	LysLeuGlyCysGlyValAlaPheAsnAlaThrValSerAlaHisPheGlyGluG	1076	Óλ
434	TCCTGGGGCACCGTGTGTGTGTGTACTGGGACACCAATGATGCCAATGTGGGTTTGCA	4285	qq
	PTrpGlyThrIleCysAspAspGlyTrpAspLeuSerAspAlaHisValValCysGl	1056	QY
428	CTGAGGCTGGTGATGGAGGTGAC	· (1)	g q
105	LeuArqLeuValAspGlyAspSerArqCysAlaGlyArqValGluIleTyrHisAspGl		δò
422	ACCTCACATGCATCAACAGCAGGATCTGAATCCAG	4183	Dρ
103	AspProTyrLeuSerAlaValProGluGlySerAl		Qy
418	GGTGTCATCTGCTCAGCCTTCCCAGTCCCAGCCGAC	4126	QQ
101	SerVallleCysThrGlySerLeuThrGlnProLe		ΟŸ
412		4066	Dp
	LeuAspAsnCysGlnMetThrValLeuGlyAlaProProCysIleHisGlyAsnThrVa	7	QY
406		4006	QΩ
975	GlyGluArgSerValArgValTrpGlyHisArgPheHisCysLeuGlyAsnGluSerLe		Qy
			Op
955	ValLeuCysArgGlnLeuSerCysGlyThrAlaLeuSerThr	936	QY
394	CTATACCGAGGCTCCTGGGGCACCGTGTGTGATGACTACTGGGACACCAATGCCAA		QQ
935	AsnValLeuGlyHisTrpGlySerLeuCysAspThrHisTrpAspProGluAspAla	916.	δy
8	TCCAGITIGGCCCTGAGGCTGGAATGGAGGTGACAGGTCAGGGCCGAGTGGAGGG	3826	pp
915	ValArgLeuValAsnGlyLysSerGlnCysAspGlyGlnValGlu	006	Qy
382	CAGCCGACACCCAGCCCAGACACTTGGCCAACCTCACATGCATCAACAGCAGGATCTG	3766	QQ
899	$R_{\rm c}$	899	Qy
376	CTCTCCCACAACTGTGGCCATCATGAAGACGCTGGTGTCATC	3706	qq
899	ProGluAspThrCyslleHisSerArgGluValGlyValVal	880	Qy
370	GATGATGTGCGCTGCTCAGGACATGAGTCCTATCTGTGGAGCTGCCCCCACAAT	3646	QQ
879	GluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCysProIl	860	QY
364	TGGGCCATGTCAGCCCCAGGAAATGCCCGGTTTGGCCAGGGTTCAGGACCCATTGT		qq
859	spalalleSerLeuSerValGlyAspHisPheGlyLysGlyAsnGl	840	Qy
358	   TGTGATGACTACTGG	3526	qq
	sAspSerAspPheSerLeuHisAlaAlaAsnValLeuCysArgGluLeuAsnCysGl	820	δλ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmskov,U., Mollenhauer,J., Madsen,J., Vitved,L., Gronlund,J.,
Tornoe,I., Kliem,A., Reid,K.B., Poustka,A. and Skjodt,K.
Cloning of gp-340, a putative opsonin receptor for lung surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 7686)
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Holmskov,U., Mollenhauer,J., Madsen,J.,, Vitved,L., Groenlund,J.,
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                                                               ValSerLeuAlaProLeuSerLys-----ThrGlySerGlyPheMetTrpValAsp 1208
                                                                                                                                                                     4870 TCCCACAACTGTGGCCATCATGAAGATGCTGGTGATCTGCTCAGCTGCTCAGTCCCAG 4929
--SerGluPheThr---AlaLeuArgLeuTyrSerGluThrGluThrGluSer 1151
                                                 CysalaGlyArgLeuGluValPheTyrAsnGlyThrTrpGlySerValGlyArgArgAsn 1171
                                                                                                                                                                                                       AspileGinCysProLysThrHisIleSerIleTrpGlnCysLeuSerAlaProTrp--- 1227
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NCQHSEDAGVICSAAHSWSTPSPDTLPTTLPASTVGSESSLALRLVNGGDRCQGRVE
VLYRGSWGTYCDDSMDTNDANVVCROLGCGWALAPGNARFGQGSGPTYLDDVRCSGN
ESYLWSCPHNGWLSHNCGHESDAGVICSGPESSLALRLVNGGDRCGGRVEVLYRGSWG
TYCDDSWDTNDANVCROLGCGWAMSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCP
NNGWLSHNCGHHEDAGVICSAAQSRSTPRPDTLSTITLPPSTVGSESSLTLRLVNGSD
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DVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSVSOSRPTPSPDTWPTSHASTAGS
ESSLALRLVNGGDRCOGRVEVLYRGSWGTVCDDSWDTSDANVVCROLGCGWATSAPGN
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CDDYWDTNDARNVCRQLGGRAMSAPGNARRGQGSGPJTVLDDVRCSGHESYLWSCPHN
CWLSHNCGHHEDAGVICSAGOSQPTPSPDTWPTSHASTAGSESSLALRLVNGGDRCQG
RVEVLYRGSWGTVCDDYWDTNDANVVCRQLGGGWATSAGNARRGGGSGPIVLDDVRC
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GDSSPFYFOGNYDTWQNWYRTWYTFRDVQLGGGCNYDYIETBYDGPRRSS
PLIARYCDGARGSFTSSSNPMSTRFTSDHSTTRRGFRAEYSSPSNDSTNLCLPNHM
OASVSRSYLQSLGFSASDLVISTWNGYYECRPQITPNLVIFTIPYSGCGTFKOADNDT
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QYGNFDVNISFYTSSSFLYPVTSRPYYVDLNQDLYVQAEILHSDAVLTLFVDTCVASP
YSNDFTSLTYDLIRSGCVRDDTYGPYSSPSLRIARFRFRAFHFLNRFPSVYLRCKMVV
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DTLPTITLPASTVGSESSLALRLVNGGDRCQGRVEVLYQGSWGTVCDDSWDTNDANVV
CRQPGCGWAMSAPGNARFGQGSGPTVLDDVRCSGHESYPWSCPHNGWLSHNCGHSEDA
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ALRLVNGGDRCOGRVEVLYRGSWGTVCDDYWDTNDANYVCRQLGCGWATSAPGNARFG
OGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASOSOPTPSPDTWP
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/protein_id="AAD49696.1"
/db_xref="G1:573598"
/translation-"MGISTVILEMCLIMGOVLSTGGWIPRTTDYASLIPSEVPLDQTV
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RLVNGDGRCQGRVEILYRGSWGTVCDDSWDTNDANVVCRQLGCGWAMSAPGNAWFGQG
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                                    Direct Submission
Submitted (16-JUN-1999) Department of Immunology & Microbiology,
Institute of Medical Biology, University of Southern Denmark,
Odense University, Winsloewparken 21.1, Odense 5000, Denmark
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="scavenger receptor cysteine-rich protein SRCR; putative receptor for SP-D"
Tornoe, I., Kliem, A., Reid, K.B.M., Poustka, A.. and Skjoedt, K.
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Matches:
Conservative:
Mismatches:
Indels:
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/map="10q25.3-26.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..7686
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2980.00
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DB:	6	23		Ę	1805
us-0	-09-759-130B-381 (1-1453) x AF159456 (1-7686)			3 8	) LI
δý	44	sSerGlyThrValGluVal 63		ζ	
Op	794 TCCAGTTTGGCCCTGAGGCTGGTGTAATGGAGGCGACAGGTGTCGAGGCCGACGGGGGT			<b>a</b> :	1805
οy	64	pasnThrThrAlaSerThr 83		Š 5	1005
qq	854 CTATACCGAGGCTCCTGGGGCACCGTGTGTGATGACTACTGGGACACCAATGATGCCCAAT	SGACACCAATGATGCCAAT 913		a	1920
ò	84	rPheArgPhe 100		QY	394
. a	o.		•	ga ,	1985
δy	101	ovalSerCysTyrGlyAsn 120		δλ	4 T 4
qq	974 GCCCAGGCTCAGGACCCATTGTCCTGGATGATGTGCGCTGCTCAGGACAC	  GTGCGCTGCTCAGGACAC 1024		qa (	2045
Qy	121 GluSerAlaLeuTrpGluCysGlnHisArgGluTrpGlySerHisAsnCysTyrHisGly	rHisAsnCysTyrHisGly 140		δ . δ	2105
Q	1025	CCACAACTGTGGCCATAGT 1084		3 8	454
οy	141		- - 24 -	음	21.65
g	1085 GAAGACGCTGGTGTCATCTGCTCAGCTCCCCA			Qy	469
οy	150		-	q <sub>Q</sub>	2225
90	1145			QY	470
y y	159 AspGlyAsnAsnSerCysSerGlyArgValGluValLysPheGlnGluArgTrpGlyThr	eGinGluArgIrpGlyThr 178 ::::		qa	2285
3 8	170			Oy	490
ž	-	13	<del></del>	QQ	2345
}	100			Οy	510
<b>3</b> 8	-	13		qa	2405
ò	219			Qy	530
3 8	-	14		Db	2465
è	5337		-	Oy	550
3 6	-		•	qq	2525
ò	255			Qy	570
7 A	1		•	qq	2585
å	250			Οy	582
3 2	-			qq	2645
3	1001			οy	588
5 5	Z/S VAIGIULGULYSTIEGINGIYALGITPG-LYINIVALCYSHISHISLYSTIPASUATA	SHISLYSILPASHASHALA 294		qq	2705
3 6	707			Qγ	608
5 5	253 ALGARIANDVALYGILVÄSLYSGILLEGUGLYCYSGLYIILLALGEUTISKIGALGGLYLGEUTISKIGALGGLYCHEU  1606 CAMPOCARANGGROCHEVARVORANGGROCHEVARVORANGGROCHEVARVARG			QQ	2765
3 6	1001			Qy	628
<u> </u>	313 FIOHISLEUGIDBEIGINOSETASPVAIRTIPLEUASPGIJVAIDEILVSSEIGIJVAI 	yvalselcysselclyash 334 		QQ	2825
λo	335			Oy.	648

5 TGTGATGATAGCTGGGACACCCAGTGACGCCAATGTGGTCTGCCGGCAGCTGGGCTGTGGC 2824 CCGACCTCACATGCATCAACAGGATCTGAATCCAGTTTGGCCCTGAGGCTGGTGAAT 2704 GCCAATGTGGTCTGCAGGCAGCTGGGCTGTGGCCCATGTCAGCCCCAGGAAATGCC 2464 5 reseccacercacccccassaarscccssTresccasssrrcassacccarrstcrs 2884 5 TGGGCCATGTCAGCCCCAGGAAATGCCCGGTTTGGTCAGGGCTCAGGACCCATTGTCCTG 2104 CysAspGlnAsnTrpLysAsnGluGlnAlaLeuValValCysLysGlnLeuGlyCysPro 413 SerAsnIleTrpAspCysGluHisSerGlyTrpGlyLysHisAsnCysValHisArgGlu 569 8 AspaspValSerCysAspGlyAspGluSerAspLeuTrpSerCysArgAsnSerGlyTrp 667 > AsnAspValSerValIleCysSer---AspGlyAlaAspLeuGluLeuArgLeuAlaAsp GlySerAsnAsnCysSerGlyArgValGluValArgIleHisGluGlnTrpTrpThrIle PheServalPheGlySerArgArgAlaLysProSerAsnGluAlaArgAspIleTrplle AsnSerIleSerCysThrGlyAsnGluSerAlaLeuTrpAspCysThrTyrAspGlyLys 5 CGGTCGACGCCCAGGCCAGACATGTCGACCATCACGTTACCTCCATCGACAGTAGGA AlaAlaValCysLysGlnLeuGlyCysGlyLysProMetHisValPheGlyMetThr 0 AspvalileValThrCysSer------GlyAspAlaThrTrp GlySerAsnArgCysSerGlyArgLeuGluValTyrPheGlnGlyArgTrpGlyThrVal CysaspaspGlyTrpasnSerLysalaalaalavalValCysSerGlnLeuAspCysPro AspLysAlaAspLeuAspLeuArgLeuValGlyAlaHisSerProCysTyrGlyArgLeu SerSerIlelleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyrGlyLysIleTrpLeu | AlaLysArgThrCysPheArgArgSerAspAlaGlyValIleCysSer-----

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Ω	<b>5</b> 0	GATGACGTGCTGCTCAGGCTATGAGTCCTACCTGTGGAGCTGCCCCCACAATGGCT	
>-	668	3 GlyasnasnaspCysSerHisSerGluaspValGlyValIleCysSerAspAla 685	
Q	2945		
>	685	982	
۵	3005	FGGTCGACGCCCAGTCCAGACACTTGCCGACCATCACCTTGCCTGCATCGACAGTAGGA 3064	
>-	989	SerAspWetGluLeuArgLeuValGlyGlySerSerArgCysAlaGlyLysVal 70	
۵	3065		
۵ ۸	3125	GluValAsnValGInGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGlyMetAsnIle 723	,
>-	724	AlaGluValValCysArgGlnLeuGluCysGlySerAlaIleArgValSerArgGluPro	
۵	3185		
<b>&gt;</b> -	₹ .	HisPheThrGluArgThrLeuHisIleLeuMetSerAsnSerGlyCysThrGlyGlyGlu 76	
۵	3240		
> Q	3305	AlaSerLeuTrpAspCysIleArgTrpGluTrpLysGlnThrAlaCysHisLeuAsnMet 783   ::	
>	784	GlualaSerLeuIleCvsSeralaHisArgGlnPro79	
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>	796		•
q	3425	CCAACCTCACATGCATCAACAGCAGCTCTGAATCCAGTTTGGCCCTGAGGCTGGTGAAT 34	
>-	800		
q	3485	GGAGGTGACAGGTGTCAGGGCCGAGTGGAGGTCCTATACCGAGGCTCCTGGGGCACCGTG 35	•
> 4	82	CysaspSeraspPheSerLeuHisalaAlaAsnValLeuCysargGluLeuAsnCysGly 83	٠
Q	4	TGTGATGACTACTGGGACACCAATGATGCCAATGTGGTTTGCAGGCAG	
, ,	84	AspAlaileSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThrTrpAla 85	
Ω	3605		
ъ q	3665	) GluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCysProIleValGlnHis 879 ::: ::	
>	880		
Ω	3725		
>-	899	668	
Q	3785		
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Д	3845		
^	916	AsnValLeuGlyHisTrpGlySerLeuCysAspThrHisTrpAspProGluAspAlaArg 935	
Д	3905		
>-	936	ValLeuCysArgGlnLeuSerCysGlyThrAlaLeuSerThrThrGlyGlyLysTyrIle 955	•
Ω	3962		

ζ O	956	GLyGluargSerValArgValTrpGlyHisArgPheHisCysLeuGlyAsnGluSerLeu 975
Οy	~	ICYSGlnMetThrValLeuGlyAlaProProCysIleHisGlyAsnThrVal 99
QQ	4085	 
QY	966	ysLeuAlaAsnValSer 10
q	4145	 
δy	1016	AspProTyrLeuSerAlaValProGluGlySerAlaLeuIleCysLeuGluAspLysArg 1035
g	4202	catcaacagcaggatctgaatccagt
y a	1036	LeuargLeuValAspGlyAspSerArgCysAlaGlyArgValGluIleTyrHisAspGly 1055
3 8		vThT] PCvsAsbAsnGlvTrDAsp[===SerAspA] aH sVa]Va]CvsG]n 107
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ó	9	ysGlyValAlaPheAsnAlaThrValSerAlaH1sPheGlyGluGlySe
Dp	4364	SECTION CONTROLL CONTROLL CARGETT CONTROLL CARGETT CONTROLL CARGETT CONTROLL CARGETT CONTROLL CARGETT
Qy	1096	GlyProlleTrpLeuAspAspLeuAsnCysThrGlyThrGluSerHisLeuTrpGlnCys 1115
QQ	4424	GACCCATTGTCCTGGATGTGCGCTGCTCAGGACATGAGTCCTATCTGTGGAGCTG
óy.	-i	erArgGlyTrpGlyGlnHisAspCysArgHisLysGluAspAlaGlyVallleCys 113
ga	4484	CCCACAATGGCTGGCTCTCCCACAACTGTGGCCATCATGAAGACGCTGGTGTCATCTG
Οy	1135	1135
Op	4544	TCAGCTTCCCAGTCCCAGCCGACACCCAGCCCAGACACTTGGCCAACCTCTGGTGCATCA 4603
οy	1136	LeuArgLeuTyrSerGluThrG
qq	4604	CTGAATCCACTTTGGCCCTGAGACTGGTGAA
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δλ	1172	IleThrThrAlaIleAlaGlyIleValCySArgGlnLeuGlyCysGlyGluAsnGlyVal 1191
qq	4718	AACGTGGTCTGCAGGC
٥y	1192	ThrGlySerGlyPheMetTr
ΩÞ	4769	GGAAATGCCCAGTTTGGCCAGGGCTCAGGACCCATTGTCCTG
Οy	1209	spileGinCysProLysThrHisIleSerIleTrpGinCysLeuSe
QQ	4829	ATGTGCGCTGCTCAGGACACGAGTCTTACCT
Qy	1228	Gluargargile 1231
qq	4889	TCCCACAACTGTGGCCATCATGAAGATGCTGGTGTCATCTGCTCAGCTGCTCAGTCCCCAG 4948
οý	1232	roAlaGl
qq	4949	CAACGCCCAGGCCAGATACTTGGCTGAC
٥y	1243	eArgvalArgGlyGlyAspThrGluCysSerGlyArgVal : :::
5	5009	<u> AATCCAGTTTGGCTCTGAGGCTGGAGTGAATGGAGGTGACAGGTGTCGAGGCCG</u>

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28 CysIleLeuLeuLeu---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC131207 202252 bp DNA. linear HTG 18-AUG-2002
Homo sapiens clone RP11-326A16, *** SEQUENCING IN PROGRESS ***, 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1260 GluIleTrpHisAlaGlySerTrpGlyThrValCysAspAspSerTrpAspLeuAlaGlu 1279
                                                                                                                                                                                          1299
                                                                                                                                                                                                                                                                                                                                                     1320 SerPheLeuTrpAspCysHisAlaLysProTrpGlyGlnSerAspCysGlyHisLysGlu 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1340 AspAlaGlyValArgCysSerGlyGlnSerLeuLysSerLeuAsnAlaSerSerGlyHis 1359
                                                                                                                                                                                                                                                                                   5185
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AC131207/c
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KEYWORDS
SOURCE
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LOCUS

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                  Direct Submission
Submitted (18-ANG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- AsnSerCysPheLeuIleSerSerPheAsnGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                       Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 194619 bases at least Q40 Consensus quality: 196802 bases at least Q30 Consensus quality: 198233 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3263 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 36871 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17393 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown length
of 5200 bp in length
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of 5575 bp in length
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of 8898 bp in length
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1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
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Matches:
Conservative:
                                                                                                                                           Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
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                                                                                                                                                                                                                                                  Center clone name: RP11-326A16
------- Summary Statistics
Sequencing vector: Plasmid;
                                                                                                                                                                                             Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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37684 c 37424 g (
                                                                                                                            --- Genome Center
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                (bases 1 to 202252)
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                               Worley, K.C.
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2	830/0	TICCAGGACAGTGGGGGACTGTGTGTGATGGGTGGAACACTACTGCCTCAACTGTC	B3OT/	
ò	82		104	
QQ	83016	GIGTGCAAACAGCTIGGATGTCCATTTTCTTTCGCCATGTTTCGTTTTGGACAAGCCGTG	82957	
ä	-		7	
ŝ	→	InrarghisciyuysileTrpLeuaspaspvaiserCysTyrciyasnciuserAlaLeu	124	
qq	82956		82897	
٥ý	125	TrpGluCysGlnHisArgGluTrpGlySerHisAsnCysTyrHisGlyGluAspValGl	144	
qq	82896	TGGGAATGTCAACACGGGAATGGGGAAGCCATAACTGTTATCATGGAAGAAGATGTTGGT	82837	
ò	145	ValAsnCysTyr	148	
QQ	82836		82777	
ογ	148		148	
QQ	82776	GAATCATCTGCTGGAAGGTAGGGGTTTCTATTATGACTTTAATAGTGTCTCTCGGGAGG	82717	
δ	148		148	
Q	82716	TGTAGGAAATATTTTATATATTCTACCCTTCCCTTATTTCCAAAGTAATGTCTAATTGCT	82657	
į				
5				
g	82656	TITCITITIATAACTATAACTGAGTITAGAAAGAAATGGAGAGAGAAAGAGAGAGACAGA	82597	
ò	148		148	
QQ	82596	GAGAGAATGCATTACAGTTACCAATGTAATATCTTTATCATAACTATAATTGAGTTTAGA	82537	
οy	148		148	
QQ	82536	AAGAAATGAAGAAGTTTGGGAGCAGGGTTAGCTTTGATTTAAGTGCCTTTTTTCATGTAC	82477	
δ	148		148	
g	82476	476 CAGGTACACTAACAGAACAATATTTCTGAAAAATGAGGTATAAAATTAAAGCAAAATG 824	82417	
ò	148		148	
g	82416	ATAAAGAATATCATGCTAATGATTGATTTTTTCACCTAGGATTTTTTTT	82357	
ò	148		148	
qq	82356	TGTGTTTAGAAAAAAGCCTCACATACCCCTCCTATAAGTATTTTCAGTTATTTTTTTA	82297	
δý	148		148	
ΩD	82296	ATTTTGGTAACTTCATTCATAACAGGGCTGTCTTCTACGTATCCTTTTGATTTTATTTC	82237	
δy	149	GlyGluAlaAs	152	
g	82236	AGGCTCAAAGTTGAATCAGTTTTTCATATGTCTGCTTGTCTTTCTCGTAGGTGAAGCCAA	82177	
à		nLeuGlyLeuArgLeuValAspGlyAsnAsnGerCysSerGlyArgValGluValLysPh	72	
3	0/170		N	
à	17	eGlnGluArgTrpGlyThrIleCysAspAspGlyTrpAsnLeuAsnThrAlaAlaValVa	92	
g	82116		82057	

80989	3 AAAAAATITCTITCTITTTACTAGGITATTTCAAAGAITTATCTTCAAGITCTG	81048	ΩD
340		340	δy
81049	) AGAATCCAAGTATTTGGTCACCTTATGGTGTCCCATGTGTTGTGCAAAGGTTTTTTAATTGA	81108	qq
340		340	QY
81109	3 ATTATITITATIAAATAAGTITITCTAIGCCAIIGICCAICTCTICTICCTICIGGAACACCC	81168	qq
340		340	Qγ
81169	] TCTTTCAGCTTCTTGTATCTGGATATCTAAGTATCTTTTAAAACCTGGAAAGTTTCAGCT	81228	qq
340		340	δy
81229	GAGTATAATGTGCCTTGGAGAA	81285	qq
340	CysSerGlyAsn	331	QY
81286		81345	qq
330	Ser	329	Qγ
81346		81396	Dp
329	AlaGlyLeuProHisLeuGlnSerGlySerAspValValTrpLeuAspGlyV	312	Qy
81397	CTGGCA	81456	qq
311	1	310	٥y
81457	GAAGACCTTATATCTCCTTCATT		· 8
0000		01010	9 6
8	aAspvalValCys	296	QY
81577	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	81636	qq
396	CysHisHisLysnAsnAlaAl	287	Ωŷ
81637	. IGNNINNINNINNINNINNINNINNINNINNINNINNINN	81696	qq
286		286	Οy
81697		81756	QQ
286	ValGluLeuLysIleGlnGlyArgTr	275	δy
81757		81816	QΩ
274	nArgCys	269	Οy
81817			· qq
569		252	å
252 81877	pasnCysargHisargGlyTrpGlyAsnHisAspCysSerHisAsnGluAspValThrLe	232 81936	oy G
81937	TGTATTGCGCCCCATTTGGCTGGATGACATTTATGCCAGGGGAATGAGTTGGCACTCT	81996	qa
232	aValLeuArgProlleTrpLeuAspAspIleLeuCysGlnGlyAsnGluLeuAlaLeuTr	212	Oy
-	GTGCAGGCAACTAGGATGTCCATCTTTTATTTCTTCTGGAGTTGTTAATAGCCCTGC	N LO	Z 6
212	]CvsAraGlnLeuGlvCvsProSerSerPheIleSerSerGlvValValAsnSerProA	192	ò

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. 80988 САСТИСТИСТИСТИСТИТАТИТИСТИТИТИТИТИТЕТИТЕТИТЕТИТЕТИТЕТИТЕТИТ		Db 79914 IGTAIGGCAICCTGGCAAGCCATTIICAGGCICACTGAAGGCICAIGAAAGIGCACAGIG 79855
.340	· ·	458CysPheArgArgSerAspAlaGlyValIleCysSerAspLysAlaAspLeuAsp
Db 80928 AIGAITICIGITIGITITITITIAIGAIAITITCITIGITGAAITICICAITAACAICCI 80869	.).	TCCCTGCTGCTGCGAGGAAGTGGGTTGCTATCAGTGATAGTGACCCCCAGACAGGTGGCT
Qy 340 340		476 LeuArgLeu
Db 80868 AAATTGTTTTTCTAATTTATTTGTATTTATCTGTGTTTTTTTGTGTGTTTCACTGAA 80809		79794 CTCAGGCTCTGGGGAGATGCTTCAGCTCTTTTATCATGGGGGAACACTCC
ОУ 340 340		487 GlyArgLeuGluValLysTyrGln
Db 80808 ATTCTTTAATAACATTATTTAAAATTATTTCAGGCAGTTCATCCATTTTCTTTTGCTG 80749		/9/43ICIGIGAACIACCCATTICCCAGIACAICAGACACIGIGIGGAAIAGAIGG
Oy 340 340		70602
Db 80748 AAATGTGGTGCTGGAGAAATTATTGTGTTCCTTTGAAGGTGTCATGTTTCCTTGCCTTTT 80689		/909Z CIGGGGACCIACACACACIGCCAGICCAGCAGCAIGGCACCACIGCAGCCCTCCAGAIG /903
Qy 340 340		
Db 80688 TATGTTCTTGTGTCCTTACATTGATATCTGTGCATCTGGTATAAAATCGTTGCTTTCAT 80629		2004   GAIRAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
341CysArgHisSerGlyThrvalAs		715 VALLY SALLANDON VALLY SALLANDON VALLY SALLANDON VALLY SALLANDON VALLA SALLANDON VALLA SALLANDON VALLA SALLA SA
80628 ATTTGGGGGTTGGCTTTCATAGAGGAAAACTTTTTGTTGTAGATATAGCTATAGTGTTGG	. ,	ОУ 520 520
348 nPhe	_	Db 79512 TGGGTCTTGGGGTTGGGGATTGGGATGTAGGACCCAGCACAAACTCCCCCTCTGGAACAA 79453
Db 80568 TTGGGTAGGGCAGTTTATCTTTGATCCTGGGTGCATGCTATAGTGTAATCTCCATGATTT 80509		Ov 521LysProMetHisValPhe 526
350		79452 CGCTATTGTGCAAACTCTAGGCAGCTCCCTGTACTAGTCTCAGAGGCACAGAAGCTGAG
80508 CTTCAGTGATAATCAGTGTGAAGAGTGTCTGGGATTTCCTCTTTGGCTTAGACTGTGGCT		Qy 527 GlyMetThrTyrPheLysGluAlaSerGlyProlleTrp539
353HisginAspAspValSerVa		Db 79392 GGGCTCTCCCATGGATTGCAAGGCCCACAGTGGGAATGTGGACTGCTAGGAATC 79333
80448 ATTAGTTAAGGCTGTTGTGAAGCTTTGCTAGGAATAAGGACACCAGACAAGCCAGTCCTT		νο 539 539
Oy 359 lileCysSerAspGlyAlaAspLeuGluLeuArgLeuAlaAspGlySer 375		Db 79332 TCTCATTTATTCTTTTTTACAGTGGGGATCCATACCAGGCTTCCAGTCAATCCTAGCCA 79273
375		ογ 539 539
C10-C20-C20-C20-C20-C20-C20-C20-C20-C20-C2		Db 79272 GACAATTGCTTCACTTCTTTCTCTCTGTGCCTCAGAAGGATCTGTTCCCTATCACTTC 79213
00.500 CAINIGCANGCANGCANIGIGNAI LINGAI CANGLICNAI ICI I GGGCI ICCANGGI GGC		Qy 540 545
VY 5/0 "	-	Db 79212 CCTGCTGGATTCCAGTGTTCTATCTTAGACACTATTCGTTGTGAAATTATCTACTTGCTG 79153
385 - Arall Bried Drive		Qy 545 545
	•	Db 79152 TITIGATCGTTTTTGGTGGTGATGTTGGGTGCTCTAGTAGCCGTCTTGAAGCCTCCCC 79093
391TrpThrlle-CvsAspGlnAsnTrpLvsAsnGluGln	-	ογ 545 545
80151 TCCCAGCCGGTATACACTGGTGCTAGCAGTGCTGGGCCAGTTCTCCAGGCCCCCAGG		Db 79092 CTTGAGCTATTCTCTTTTAAGGGAAAGTTCTTCTCCCATAATCATGAATATCAATGTGT 79033
Qy 403AlaLeuValValCysLysG 409		545
Db 80091 TGCCACATGTAGGTGGTGCTGGAGGTAGTGGTGGCACCCAGCAGTGCAGGTGCAGGTTCTGTCCTC 80032		79032 CTTTCAATAAGAGAGTTGAGGATTCCTGAACACGGGACCCAACTCCAATCCATAGAAAACT
Oy 409 InLeuGlyCysProPheSerValPheGlySerArgArgAlaLysProSerAsnGluAlaA 429		Oy 546
Db 80031 AAGGCTACTGATGTTGCACACGGCACAGACTATGGTGAGTGGAATAGGGCAATTTC 79975		703/2 BCCCBCBCCC111C11C11C1C1C11C1C1C11C1C1C1C1C1C1C1
Oy 429 rgAspileTrplieAsnSerIleSer-CysThrGlyAsnGluSer 443		747, 765164   11   1   1   78912 TAATAATTGTATATATATATATATATATATATATATATA
79974 CAGACCITIGGGIGGCAIGCITAGGIGGIAGCAGGIGGGCAAACCICCAIGIAGGICCI		549
Ov 444AlaLeuTrpAspCvsThrTvrAspGlvLvsAlaLvsArgThr 457	_	

78852 TAAAAATAATATATATAAAAACAATTATATATATAAACAATTCTATATAAAACCATTATAT
78792 ATAAATATATAATTATGTATATAAAACAATTACATATAAATATATAT
549
78732 AAAAACCTAAAAGTCAATAIGAIGICACCTITITIAIGCIGAAICACCIACAGCAACIGII
549
78672 TITCCACCIAAGACICTCTCTCAGAGIGGAATAIGIIGCIACAAAGCAGIGAAAIAIGII
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78612 TITCCCTTATATTTAGAGTAGTICATTTAATGAAGAAAGTTCATCTGTTTCTAGACACCT
563
78552 ITTCAGGGAATCTCAATTTTGATAGAGATTCCTACAAGATATATAT
563
78492 CCCTCCCCACCACCACACACAAAATTATAGCTCTCTAAACGTCAGTATCTAAAATAAACC
564ASBCySValHisArgGI 78432 CCATTTAAAAAAATTCTTTTATGGTAAAGTTGCTAAGACTGATCTACCACCC
569AspVallleValThVCvsSerGlvAspAlathrTrnGlvfeArpValVSe
b AAACAGATCTTGACT
393SetGlyalguediudaliytrhecholyalarip
004
78216 TTTAGAGAATCATCTCATATCTACACAAGATTATATCAAAATAACCAATGTAGTAAAATT
605
612
78097 TITCCAGGTCCTCTAGACCACGITAATITATTTTTTTTTT
612
78037 TAACTTGGTCAGGTTTGATCTGGTCAAAGTCAGAGTTGATTTTCTGACATGTCAGATCTG
612
77977 TCAACATTAGGCAGTTAATAAACCTATTAATATATATTTAGTATATAAAGTAGAAAAATAG
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77917 TATGATATCACATAGACATTTAATAATGGGAATTTTTATTTTTAACTAAAACAATAGAAA
//05/ AGAMOCICAINTINIANIIIIIIAAIIAGAAAAAAAAAAAAAAAAAAA
070
77797 TAGATATATTCTCAAATTAGTAGGCAATATTATTTGTGTTTCACAGACTATGCCACAGCA

οy	626		929
gg	77737	CACTCAAAGCTACCAAACTGCCCTAAAAAGATAAAGTAACCTTTCTAGAATGAGATTCAT	77678
Οy	626		979
qq	77677	TTCATTTTATGTCAATACTGCTAAAAATTTCCTTCAAAAGCTGACTCTTTCAATTAGGCT	77618
ΩŊ	626		979
QQ	77617	CAGAATTAAATTTCTGATTTAATTCTTCGTTTCCTCTTTTTTAAAAAGTTTTTTATTTCCA	77558
Οy	626		979
QQ	77557	TAGGTTTTTAGGGAACAGATGGTAATAGTTACATGAGTAAGTTCTTTAGTTTGATTTGT	77498
Oγ	627	Proserser	629
qq	77497	GAGATTITGATGCACTCATCACCCCAAGCAGTATACACTGAACCCAATTIGTAGTCTTTTC	77438
δy	630		633
QQ	77437	TICCTCAAACCCCTCGTACCCTTTCCCCTGAGTCCTCAAAGTCCATTGTATTTTTTTT	77378
δλ	633	tGlyLeuGlyAsnAlaSerThrGly	641
Db	77377		77318
οy	641		641
ор	77317	TTCCATTCCTGAGTTACTTCACTTAGAATAATAGTCTTCAATTCCATCCA	77258
QY	642	TyrGlyLysIleTrpLeuAspAspValSerCys	652
qq	77257	AATGCCATTAATTCATTCTTTTATGGCTGAGTAGTATTCCATCTGTATATATA	77198
ΟŊ	652		652
Ob	77197	CACACATACATGTGTGTATACGCATATACACACATACATGTATGT	77138
δλ	652		652
QQ	77137	CATACATGTATACGTGTATACATACATATATGTATGTATATGTGTATATGCACACACA	77078
δλ	653	AspGly	654
qq	77077	CACACACACACACACACCACAGTTTCTTTATCCACTTGTTGATTGA	77018
οy	654		654
qq	77017	CTGGTTCCATATTTTGCAATTGCGATTTATGCTGCTATAAACATGCGTGTGCAAGTATC	76958
οy	655	AspGluSerAspLeuTrpSer	661
οqα	76957	TITITCAGATAATGACTTATITTCCTCTGGGTAGATACCTAGTAGTGGGATTGCTGGATC	76898
Qy	661		199
QQ	76897	AAATGGTAGCTCTGCTTTTAGTTCTTTAAAGAATCTCCACTGTTTTTCATAGCGGTTGTA	76838
ΩŊ	662		664
QQ	76837	CTAGTTACATTCCCACCAGCAGTGTAGAAGTGTTCCCTTTCCACTGCATCCATGAAACT	76778
δλ	665		999
q	76777	CTATTCTTTTTTGATTTTTGGTTATGGCCATTCTTGCAGGGGTAAAGTGGCATTGCATT	76718
δy	999		999
g	76717	GIGGTITTGATTTTCCTGATCATTAGTGATGATGAGCATTTTTCATTAAAAAA	76658

Qy	999		999		_
qq	76657	/ AAAAAACTTACCTACTCCTCTCTCACATACAGTGAATTTTGTGTTTTCTTTTCCCGAGC	76598		
Qγ	667	77   TrollyAsnAsnAspCysSerHisSer	675		
g &	76597	7 TCCAATTTCTTTTAGAATTACTTCATTTGGCATCACTAATAGGCAAGTTTCTCCCATTTT	76538		
q	76537	7 TCTGGATTTGGTAATATCACAGCCCTATGCAGTTTTTCCTTGACTTTTCATTAAATTATA			
δ	675		675	•	
qq	76477	7 TCACCTCTTCCTAACATTCTCTTTAGTATCTAACATGTAATATGTAATTCTTCAAATATT	76418		٠.,
ΟŸ	929		619		
QQ	76417	.::::::::	76358		
Qy	619		6.29		
qq	76357	7 TTGTAAGTAAAACTATATCCTTGCTTTGTAAGCCAGAAATGTTCATGGATTGAAACATAC	76298		
δλ	619		619		
qq	76297	? CTTGGTGTACTTTTGTTATTTTTTTTTTATCCAATAAAAGGAAAATTAAGTTTGAAGG	76238		•
οy	619		629	•	
qq	76237	7 AAAGTAAAAATAAAATTAAACACTGGTGAAGCCGGGACCTAAACAATCTCTCAACTTTT	76178		
Qy	619		679	٠	
qq	76177	' GGCCACTGGTCTATGTTAGTGTACAGGAATGGATAAGAATCTTTAATGTCTCACATAGAG	76118		
Qy Db	680	)	692 76058		
Qy	692		712		
qq	76057		75998		
Qy Dp	712 75997	YILELeuCysAlaAsnGlyTrpGlyMetAsnIleAlaGluValValCysArgGlnLeuGl 	732 75938		
ò d	732	ucysGlySerAlaileArgValSerArgGlubroHisPheThrGluArgThrLeuHisll 	752	•	
3 6	1		6 (	-	
oy Oy	752 75877	<pre>2 eLeuMetSerAsnSerGlyCysThrGlyGlyGluAlaSerLeuTrpAspCysIleArgTr                                      </pre>	772 75818		
Oy Dp	772	PGluTrpLysGlnThralaCysHisLeuAsnMetGluAlaSerLeuIleCysSer	790 75759		
ΟŊ	. 790		190		
QQ	75758	ATTICIGGACAAAGATAAACACATTTATTTAATTATTTATTTTGCACTTATTAATACG	75699		
οy	790		790		
QQ	75698	) TGTTTATGAAGTGGCTATTTAACAGTATTAGGTCAAAAGTAAATGAACTAGATAAAAGTA	75639		
δλ	790		190		
ор	75638	) ATCCTACCCTCTATCTAGAAGACAGGTATATAATAAAAATATATAATTAAATAACTGTTT	75579		
Qy	790	,,	790		_

qq.	75578	ATTTAAAATTGCGTGAAGTAGAAGCACAAGATGAAATGAGAAGGCATAATTAGAAGATAT	75519
Qγ	790		790
QQ	75518	TACCTATTTGCAGAGTCGGAGAATATTTCTGTGAAGTGATAGTTAAGGAAAGATGTGAAG	75459
Qy	790		190
qq	75458	GACAGGTAAGATTTAATCATATGAAGAAGTGTTGGGAAGATTAATTTAAACAGTAGTATT	75399
QY	790		190
qq	75398	TTATTCGAGTAACACACCTGGGAATAAGCTTGTGTTATTCCAGGAACTAAAAGATGGTTG	75339
Qy	790		190
qq	75338	AAAGAAGAGGTATTAGATCCAAGTGAAGAAGGGGGAAAAACTTATAATAAAGTCTTGATAT	75279
Oy.	790		190
ΟQ	75278	GTAGGCAAGGGAAAGGTTATTTATGGAGTAGGAATTGTGAACTTTATTCTAAAGTGAATG	75219
QY	790		190
qq	75218	ATAAATCATTGAAGGTTGTAAGCATGATACAACTTGCATTTCAAAGÄCAGCACTCTGGCT	75159
ΟY	790		190
qq	75158	GCAGTGTGGGGTGTGTGTGTTTTATGTGTGTGTCTGTGTGTG	75099
δy	790		190
qq	75098	GCTATTGGATGCCGGGAGTCATGCTGTTGAATAATTCTAGGGAAGATACGGAATTTTGAT	75039
Qy	.790		190
q <sub>O</sub>	75038	TAGGATGCTCACTGTGGAGCTGGTGAAAAGCTTCCAAATTTCAGAAATATTTAGTAGCTG	74979
QY	790		190
ΟD	74978	AAACCAGCAGAACTGAATACACTGAATGTGGAAATAAAGATAAAGGTTTCTAGACTAAGC	74919
QY	190		190
QΩ	74918	AGATGGGTGCACTGCAGTGTCATCTGGAAAGATAATCTTGGAAGAGGAGCAGTTAAG	74859
, δy	790		190
qq :	74858	AGAGGGTGGGATGATGAGTCCAATTTTGTATGTGTGAAATATGAGGTAATAGGAAGCAG	74799
QY	790		190
QQ	74798	TCATCAAATGAAGAGGGTTGGAGGAAATTGGATATGAGATTTAGATGAT	74739
δy	790		190
Dp	74738	TATTGAATGGAGATATAACTATTAGAGTCCTACATATGTAGACGGAAACTAAATCTAGGA	74679
QY	790		190
QQ	74678	ATAAAATGTAAATTGAGAATTTTTAAAGCCTAGATTCAAGAAAGA	74619
QΥ	790		190
Dp	74618	GAGGAACAATAGTATTTAATAGTTTATTGACATAAAAGAAGTTGGAAAAGCATACTGAGG	74559
QY	790		190
qq	74558	AACAGTGGTGGCAGAATGTCACATCGCTAAAGCCAAGGGAAGATGTTTCAAAAAGATGGG	74499
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δy	790		790
qq	73358	ATAAGAAATCCAAATGGAAATGCTAAGTAGAAATTGGATAAATGAGTCAGGAGTTTGGAA	73299
οy	790		190
Dp	73298	AAATGCCTGGGTTGGAGACAGATAACATACATTACTAATATAAAGTAGCTTTGCTGCAAAG	73239
δy	790		190
QQ	73238	AATAGAGTCAGAATAATGGGCCAGTATTTTTTTTTTTTT	73179
οy	790		190
qq	73178	ATTGCTGGGATCTAACCAGTAAGTAGAAGTCTTTCTATTCTTATATTACACCATCTTCTT	73119
δy	790		190
qq	73118	AAGATGACTACAAAATCTTCACGTGTTGTTTAATGCTGAGGTTACTTAGTATTTTTTAAT	73059
δy	790		190
Dp	73058	GTAAACAAATTGTGCAATTCATTTCCTTCTGATGAGTTCTAAATCTAGGATTGGTGGGTC	72999
οy	790		190
QQ	72998	ACCAAGACATAGAAAATAGGTATGTAATCCAGATCTGTGAATTTAAGTCTGTACTGCTAA	72939
δλ	790		190
QQ	72938	TCTTGTCCTCTGAGCCCCTACGAATGGGATGTTCTAATGATGAATGGAGAAAATTGCTC	72879
Qγ	790		190
Db	72878	TGGGGTTAGATATGGAGACTGGAGACAGGGATAGATATTGGAAAAACCCTAAAAACTAAACC	72819
οy	791	aHisArgGlnProArgLeuValGlyAlaAspMetP	804
qq	72818	CAGGCTGGTTGGAGCTGATATGCCCT	72759
Qy Db	804	sSerGlyArgValGluValLysHisAlaAspThrTrpArgSerValCysAspSerAspPh 	824 72699
Qy	824	erLeuHisAlaAlaAsnValLeuCysArgGluLeuAsnCysGlyAspAlaIleSe	844
QQ	72698	TCTTCATGCTGCCAATGTGCTGTGCAGAGAATTAAACTGTGGAGATGCCATATCT	72639
δy	844	ServalGlyAspHisPheGlyLysGlyAsnGlyLeuThrT	864
qq	72638	CTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCAGT	72579
Οy	864	isLeuAlaLeuCysProIleValGlnHisProGluAsp	884
qq	72578	<u>addeadtgaaactcaccttgcattatgccccattgttcaacatccggaagacactt</u>	72519
δy	æ	IleHisSerArgGluValG]yValValCysSerArg	96
qq	72518	TCCACAGCAGAGGAGGTTGGAGTTGTCTGTT	72460
δy	968		968
qq	72459	TGGCTGGGGCTAGAGATGGGGGAGTTTGGGGCTGGAGGTGATAAGTCATGATGTCTTTCT	72400
δy	897	spValArgLeuValAsnGlyLysSerGlnC	606
qq	72399	ACAGATGTCCGACTTGTGAATGGCAAATCCCAG	72340
δ	606	sAspGlyGlnValGluIleAsnValLeuGlyHisTrpGlySerLeuCysAspThrHisTr	929
QQ	72339	TGACGGGCAAGTGGAGATCAACGTGCTTGGACACTGGGGCTCACTGTGTGACACCCACTG	72280

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PASPProGluAspalaargValLeuCysArgGlnLeuSerCysGlyThrAlaLeuSerTh 	rThrGlyGlyLysTyrIleGlyGluArgSerValArgValTrpGlyHiSArgPheHisCy 	SLeuGlyAsnGluSerLeuLeuAspAsnCysGlnMetThrValLeuGlyAlaProProCy 	s _	TATCCATGGAAATACTGTCTGTGATCTGCACAGGTAAGAGAATAGTGCTTATGGTTA	CTACTGTCAATATAGCCCAGACATGGTAGAGGGAGTTGGGGTTAAAGGAAAGATGGT		GAAAATGGGGGTGCAGGTGGAGGGGGGATAGGCATGACAGTC		AATAATGATAACTAGGACCATTCCTAAGGGGAAGTTAACACCTCTGTGTTTGGGATTTAC		GAGTAGACATCATTAATAAAAATGATTTCAATAGACGACAG		ACAATTGCAGATTCCATGTTGTTACAGAACTCTTCAACCTT		ACTITIGCCCCATITCCTGCACCTCCACGAGGAAGCCTGACCCAGCCACTGTTTCCAT	SLeuAlaAsnValSerAspProTyrLeuSerAlaValProGluGlySerAlaLeulleCy		   CTT-AGGTAAGCAGAATCAGTTTTAGGAAACACTGCAACTCTAAAGAATGTGACCTAT		ACTGGACTTTCTCCTCTAAGAGGACAAACGGCTCCGCCTAGTGGGATGGGGACAGCCGCT	sAlaGlyArgValGlulleTyrHisAspGlyPheTrpGlyThrIleCysAspAspGlyTr	TGCCGGGAGAGTATCTATCACGACGCTTCTGGGGGCACCATCTGTGATGACGCTT	PASpLeuSerAspAlaHisValValCysGlnLysLeuGlyCysGlyValAlaPheAsnAl 	aThrValSerAlaHisPheGlyGluGlySerGlyProlleTrpL		SThrGlyThrGluSerHisLeuTrpGlnCysProSerArgGlyTrpGlyGlnHisAspCy	CACAGGAATGGAGTCCCACTTGTGGCAGTGCCCTTCCCGCGGCTGGGGGGCAGCACGA	SArgHisLysGluAspAlaGlyValileCysSér	CAGGCACAAGGAGGACGCAGG	
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qa	71200 CCT	CTACACACACGTGCACACACTTGCACACACACACACAATTGTAAAGTGTAGTGAAA	71141
QY	1136		1136
qa	71140 AGT	GTATGGCCTAGGAATACAAAAAAAATCCACTTGGTTTTAATCCTATTCTCTTATA	71081
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qq	71080 CIGAT	TTCTTAATACCCTTGTCATATTACATTTGTCTGGGTATCATTCAT	71021
QY	1136		1136
qq	71020 AAT	AAAAGATTGGTCTTACTGTCAGAGAATGTTAGACCCCAAGAAAGGGACCTTACATGA 7	70961
QY	1136		1136
qa	70960 CAT	CATCCACTCTGGCTCTGAGAACACACTGTCAACCGTGTCCAATCTGCCTTATTTTGTTGT	70901
QY	1136		1136
qa	70900 TTT	TTTGTTTTGTTTTAGGCTTTTAGCTAGCCTGAAGCCATGGTTATTAGTTTCTGTCT	70841
νο	1136		1136
qq	70840 CTA	CTAGTGGTAAGAGGAAAGGGATGAGGAAGGGTCTTTACTAACCTGACCAGAAGCAGAA 7	70781
QY	1136	[	1136
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QY	1136		1136
QQ	70660 TTA	TTAAGTTGATACAAATTTAAAGCTCAAATACTATTCTTGGGAAACCCACACTCATCCTGA 7	70601
Οy	1136		1136
qq	70600 AAT	AATCTTACAAGACCCTTAGTTTCCATCAGATTTATGCTGTTAATATGTTAGAGTGATTTA 7	70541
οy	1136,	[	1136
QO	70540 TGA	TGAAATTGTATTGTGAGCCCTAATGTATTATTTCCATGGGAAAAATGGATTCCTTGGGGA 7	70481
QY	1137		1138
ΩD	70480 GGG	GGGATTTTCCAACTCCAAAGGAAATATTTAATACTAAGTTTTGTATTTCTCTGTAGAATT	70421
QY	1138 eTh	eThrAlaLeuArgLeuTyrSerGluThrGluThrGluSerCysAlaGlyArgLeuGluVa	1158
Db	70420 CAC		70361
QY	1158	IPheTyrAsnGlyThrTrpGlySerValGlyArgArgAsnIleThrThrAlaIleAlaGl 	17
QQ O	70360 CIT		70301
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Oy 1243 1243	1243
Db 70060 AATATAACTTACCATAAATAGCAAATCTTTCCATTCAGGAGCACATGGCAGACTCACTGA 70001	68980 ACACAGACATACATACCTTCCCAAATTAAAATTTCACCTAAATCAACATAATTTGCAT
Oy 1243 1243	1243
Db 70000 AAAGTGCATGACAATAAATGCTGATTTATCGCATCTGTTCTATATTGAAATTTTATTATT 69941	O SGGTTTGGTTAGTAGTGGATATGGACATTATTTATGAATATTGTCTGTTTGTGGTTCATA
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Qy 1243 1243	1243
Db 69880 CTCCTTGTGAGAAGCTGGATGAAAGCACATAAAAGGATAACAACACATAAAAAATTACAG 69821	CAAACAAAAAATTTGAAAAAAACCCAGAAATCATGGAAAAAAAA
	Qy 1243 1243
69820 TGTTTTAAAAAATGAAAATATAATATGTATACTGTCTTAGAAATTCTAGAAAGCTCAGA	68740 ATACCATGATCAGTTGATGATATATAGCTGATATTACACTCTTGAGTATCATATGTGT
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Db 69640 TTAAAATTTAATATGTTTTTTGTAGAGATTTTAGAAATTGTACAATTATAAATAA	Oy 1243 1243
Oy 1243 1243	68500 TATTTTCCATTTAAGTAACGTCACATTAAATATCCTTAAATATATAGAAAATTATTT
Db 69580 TGCATTCCACGTTTAATCTGATTATCAAAATAACCATTACTAATATCAGAAACATTAA 69521	277
Qy 1243 1243	1743
Db 69520 CTATTAGTCTTCCTTTTGTACAAAACTTAAAGTTATGATTGTGTATGAAATGTGTAT 69461	68440 AAGCANATTICICAANATTICITCCCAAAANCIATTITCCNATTIGAICAANTANATA
Oy 1243 1243	1243
Db 69460 ATGAAATATAGATACTATATATGTATATATATATATATAT	Db 68380 CCTGAAATTTTGGATTTCAACTATCTTAAGTTTTAATTTATCAATATTTATATAAAAA 68321
	. Qy 1243 1243
60400 III AMAMAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Db 68320 TTTGCATCTATATGTATATGAATGATACTATGCAGTAGATCTTATTTAGCGCTCTTTTA 68261
05400 IAGICITACACIAIAITIAGGAIAICIGIAICITACITITAIAIGIAAAAGIAIACIGIA	Qy 1243 1243
1243	Db 68260 TATTGTTGATATTAGCATTGGAGATTTGCTGAAATATAAACTAGGATGAATTCTGCCAG 68201
69340 AATATTCTAATTCCAATGAATAGCCTTCAAATGGCATACAATATTTATCATGTGAAC	Oy 1243 1243
Qy 1243 1243	Db 68200 CTTTATGATCTTTAATAGTATATGGAATAAAATCATTGTGTTTCAATATTTGAAAGAGA 68141
Db 69280 ATAAATAACCATGTGATTATTGGTATTAAGGCTATTTCTCAATGTCAAACTAGTATAAAT 69221	1040
Qy 1243 1243	C+7T
Db 69220 AATGCCATTATAAGCATCCTTATTCATTTTCGGTGAATCTCTGATTATATCTGAAGGTTA 69161	68140 ATAACTATAGCTATTTTGGGTAGTAATTTGTTAATACTTAAAAAGAATGTCCAGGACTAT
Qy 1243 1243	
Db 69160 TATTTCTAGTCCCAAAATGAGTGGGTAAAATGAGTGAACATTTTTATGATCTTTATATG 69101	Db 68080 rgccttattctcattttcttgagtcaattttgtgaaaggatgaaagaatgtattagtcag 68021
Oy 1243	Oy 1243 1243
69100 TACTAGTTAATTGCTCCAGCAGAAGCCTATGTATTAGTTTTCATTCTTATCCCCAGTAT	Db 68020 TTCTCATGCTGCTAATAAAGAAATACCAGAGACTGGGTAATTTATAAAGGAAGG
	Qy 1243 1243
######################################	Db 67960 NATGGACTCACAGTTCCATATGGCTAATGAGGCCTCACAATCATGGCTGAAGGCAAAGGA 67901
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. 6	_	GGAGCAAAGTCACATGTTACATGTGGCAGGAAAAAGAGAAAAAGAGAAGAAGAAGAAAGA	67841	qq	66820 ATT
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ΟY	1243		1243	<u> </u>	
QQ	67660 AAAAACC	AAAAACCATACTCTGAATTTATTATTATAGGCCATTCAATGATGCACTCTGTATTGGT	67601	අධ -	66580 CAT
οy	1243		1243	δ	
qq	67600 AGGAGGT	<b>AGGAGGTAGAAGCTAGTCTAAAAGTATTTAATGAGCAGGAGATTTACAAAAATGACG</b>	67541	<u>අ</u> ධි	66520 GTT
Qy	1243		1243	. Oy	
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qq	67480 GGAGAGG	GGAGAGGGGCTCTTATGACAAGGAGAAAGGAAATTTTTAAAAGGGTGCATGTGAAAGTTA	67421	<u>අ</u>	
· 0y	1243		1243	QY	
qq	67420 TCAGGTT	TCAGGTTTGAGGACTTGGGGATGACTTATCAGACCGGGGGATGAGACGTTTAGATCAAAA	67361	අධ	
QY	1243		1243	δ	1300
qq	67360 AAACCCT	AAACCCTTTTGAATAGAAGCCAAATTACCTAAAAGTTAATTATGTACTGAAACTGTAACT	67301	<b>q</b> a (	66280
Οy	1243		1243	λο 1	1320
QQ	67300 TITCCIA	TTTCCTATACTATTACGGGAACTAAAATCCAATAGAGAAATCCCGAGATTCTCTTTTGGT	67241	gg .	66220
οy	1243		1243	Qy	
අ <u>ධ</u>	67240 CTICATG	CTTCATGTGGTTGGTGGCAGAGGTAAGGCAGAGGCTTAGAATATGAAAAAACATTTAAC	67181	<b>අ</b> ධ	66160 TGC
Qy	1243		1243	оу 	1345
QQ	67180 AAAATAA	AAAATAATAAAAGAATGAAACATAAAAATGTTAAGATCATTCTAAAATATTGAGGATCCTG	67121	gg .	Ð
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qq	67120 CAGACTT	CAGACTITITIGGCAGCAAGTITAAAATGACCCCGGTTATAATTATCTGCAGTGAACTC	67061	qu io	D.
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. · d	67000 AGCCATG	67000 AGCCATGTGACGAGAGGTCACTAGTGCCAAAGCATTGTTCATTTGGGAAAGAGAGTGTTT	66941	qq	w
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QY	1243		1243
QQ	66760	ATAGGACACTGAAATTTGGAAAATGAAATCAATATGTTTTGTTTTCAAACATCTAGAGTA	66701
QY	1243		1243
QC	00299	AATGAATATCTGGTTTGGCCTCGCTGGAGATG	66641
QY	1243		1243
qq	66640	CAAACCACAGTCATGTATAGGGGTTTATTCACTTCACAGGTTCTTGTCTAATCTATGTAA	66581
QY	1243		1243
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QY	1244	AsparglleargValArgGlyGlyAspThrGluCysSerGlyArgValGl	1260
qa	66460	ATAAGAGTGCGTGGAGGAGACACCGAGTGCTCTGGGAGAGTGG	66401
QY	1260	ulleTrpHisAlaGlySerTrpGlyThrValCysAspAspSerTrpAspLeuAlaGluAl	1280
qq	66400	ATCTGGCACGCAGGCTCCTGGGGCACAGTGTGTGTGATGACTCCTGGGACCTGGCC	66341
Qy	1280	aGluValValCysGlnGlnLeuGlyCysGlySerAlaLeuAlaAlaLeuArgAspAlaSe	1300
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qq	66220	GAGTGACTGTGGACACAG	9
QY	1340	ValArgCys	1345
qa	66160		66101
Qy	1345	1	1345
qq	00199	TGGTAGAGAACACTGGGAAACAGGCTCACTCAGAGAGTTGAGCTGAAGATACTAGG	66041
Qy	1345		1345
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Qγ	1345		1345
qu	65860	GAGATGTTAAAAGGATATTTAAATGACATCCGATAATCGCAGGAGATGTAAAAAAAA	65801
Qy	1346	SerGlyGlnSerL	1350
qa	65800	CAGGACAGTCG	65741
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δy			Qy 1395 1395
qq	65500 TCTCATGGTACCCTCATAGATAATCTTTCTAGATTCTCAAATATTCTTTATGAGACTGGC 65441		Db 64421 GATAATAGTCTTACCTCATCAGGTTAAGATAGTTAAAATAAAT
ò	1357 1357		Oy 1395 1395
qq	65440 AGAAACAGCTCAAGCTTCAGGÀGAATCACTTAAACCCAGGAAGCAGAGATTGCAGTGAGC 65381		Db 64361 AAAATGGCCAGCACATAGTAAATACTATGTAAAGAACTTGGTAATAAAAGTGGAAGAATA 64302
ογ	1357		
q	65380 CGAGATCGTGCCAGTACACTCAGCCTGGGTGACAGAATGAGACTCCATCTCAAAAAAAA		64301 ICAAGGAGAAAAAGGAGGATAAATTTTAAAAATGTAAAAATTCACTAGCAGGGGTAGG
δ	1357 1357		
q	65320 AAAAAAAAAAAAAAAAAAACAGCTCAAGCCCTAGTATTTCTGATTCTGGTGTTTTAGT 65261		64241 FGCTGAAAGAGCCATTGGATTTTAGCTCAGAGGGATTAATATGTGTCAAACCTTAGCATT
ογ	1357 1357		1395
g	65260 AGTGAATGCAATGCAAGAGGAAAGGTTTAGTTATCAAATCTCTTGTATAAAATTGGAAGT 65201		Db 64181 AAGTGTCCTAATATAAGGGATAGGCCATTTGAATTTGAATCCTAACCATGAAGCATCCAT 64122
δ	1357 1357		1396SerThrArgArgArgGlySerLeuGluGluAsnLeuPheHisGluMetGluT
g	65200 AATTTAGGGCAATAGAATTATGGAAAGATTTGGATTCAGTTGTTCCAAGATAGTTTCAT 65141		64121
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Q29111 sus scrofa Q90000 strongyloce Q29110 sus scrofa Q29110 sus scrofa Q29112 sus scrofa Q29112 bus scrofa Q28910 bos taurus

Q29113 sus scrofa

091v20 oryctolagus 091v21 oryctolagus 091v2 oryctolagus 096180 homo sapien 091vn8 mus musculu 091wn5 mus musculu 091wn5 mos sapien

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Gaps

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Indels

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1 NMLPQNSWHIDFGRCCCHQNLFSAVVTCILLLNSCFLISSFNGTDLELRLVNGDGPCSGT 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gronlind J., Vitved L., Lausen M., Skjodt K., Holmskov U.; "Cloning of a Novel Scavenger Receptor Cysteine-Rich Type I Transmembrane Molecule (M160) Expressed by Human Macrophages."; J. Immunol. 165:6406-6415(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Scavenger receptor cysteine-rich type 1 protein M160 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1453;
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EMBL. AF264014; AAF91396-1;
EMBL. AF264014; ASF01396-1;
Enterpro: IPR001190; Srcr_receptor.
Pfam; PF00530; SRCR; 12.
PRINTS; PR00258; SPERACTRCPTR.
SMART; SM00202; SR: 11.
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159263 MW; 15445CE9868CF58A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last seq
               Q9JMJ9
Q9NC87
Q95JE5
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Q96180
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Q91WN5
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Q92098
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PROSITE; PS50287; SRCR_2; 12.
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098TD1
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Q29113
Q29111
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Q95JD9
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Best Local Similarity 99.7%;
Matches 1449; Conservative
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Q9y4v9 homo sapien
Q96943 geodia cydo
Q95218 oryctolagus
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            GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                 671580 seqs, 206047115 residues
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                                                                          protein search, using sw model
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qq	QV Db	OY Db	Oy Db	OY Db	QY Db	Oy Dp	RESU 0078 ID	DT	00 00 00 00	OX RR RA RA RA	RA RT	DR DR	DR DR	FT FT SO	W B C	. Qy Db	Qy	Qy
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	1 VEVKFQGQWGTVCDDGWNTTASTVVCKQLGCPFSFAMFRFGQAVTRHGKIWLDDVSCYGN	1 ESALWECOHREWGSHNCYHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTIC	1 DDGWNLNTAAVVCRQLGCPSSFISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWG	1 NHDCSHNEDVTLTCYDSSDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVC	1 KQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVI 	1 CSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSR 	1 RAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVG 	1 AHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPINL 	DDVSCIGNESNIMDCEHSGMGKHNCVHREDVIVTCSGDATWGLFLVGGSNRCSGRLEVYF 	1 OGRWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLW	1 SCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWG	1 MNIAEVVCROLECGSAIRVSREPHFTERTLHILMSNSGCTGGBASLMDCIKWEWRQTACH	LINMEASLICSAHROPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGD	AISLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDV	RLVNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSV 	RVWGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLS	AVPEGSALICLEDKRLRLVDGDSRCAGRVEIXHDGFWGTICDDGWDLSDAHVVCQKLGCG 	VAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTA
1	61	121	181	241	301	361	421	481	541	601	661	721	781	841	901	961	1021	1081
a	Qy Dp	Qy Dp	Qy Db	Qy Db	Qy Dp	Qy	g g	Oy Db	Q D	oy G	Oy.	Qy Dp	QY Db	oy Db	Qy Db	Qy Dp	Qy Db	Qy

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1201 GSGFMWYDDIQCPKTHISIWQCLSAPWERRISSTAEETWITCEDRIRVRGGDTECSGRVE 1260
                                                                                                                                                                                                                                                                                                                           1261 IWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGGGTGTIWLDDMRCKGNES 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.3%; Score 3441.5; DB 4; Length 1151; Sest Local Similarity 55.2%; Pred. No. 4e-260; Atches 608; Conservative 166; Mismatches 311; Indels 17; Gaps
                                                                                                                                                                          1201 GSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGGDTECSGRVE
                                                                                                                                                                                                                                                                                             1261 IWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNES
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-NAR-2002 (TrEMBLrel. 20, Last annotation update)

M130 antigen cytoplasmic variant 1 precursor.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

        SIGNAL
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        40
        POTENTIAL.

        CHAIN
        41
        1151
        M130
        ANTIGEN CYTOPLASMIC VARIANT 1.

        SEQUENCE
        1151
        Aa, 124820
        MW; 3CD0BAD857B6EB91
        CRC64;

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Eur. J. Immunol. 23:3320-2325(1993).
EMBL, 222969; CAA80542.1;
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00530; SRCR; 9.
PRIWTS; PR002258; SPERACTRCPTR.
SMART; PS00420; SRCR. 1; 4.
PROSITE; PS50287; SRCR. 2; 9.
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NMCSGRIEIKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWFDD 220
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                                                                                  RNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMN 722
                                                                                                                  723 IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN 782
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                        VNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRV
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                                                 RWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSC
                                                                                                                           MEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAI
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Last sequence update)
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007898;
01-NOV-1996 (TrEMBLrel: 01-NOV-1996 (TrEMBLrel: 01-NOV-1996)
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                                                                                      Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1116;
                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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W; E805BC80B52E4009 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Ritter M., Buechler C., Langmann T., Schmitz G.;
"Genomic organization of the human CD163 gene.";
Submitted (NOV-198) to the EMBL/GenBank/DDBJ databases.
EMBL; 222968, CAR80541.1;
EMBL; X18389; CAR85233.1;
EMBL; X18389; CAR45233.1;
EMBL; X18390; CAR45233.1;
EMBL; X18390; CAR45233.1;
EMBL; X18391; CAR45233.1;
UJOINED.
EMBL; X18392; CAR45233.1;
JOINED.
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20, Last annotation update)
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3.7e-259;
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SEQUENCE FROM N.A.
MEDLINE=93380506; PubMed=8370408;
MACALINE=93.4051; Shaw J.M., Zhang X.P.,
Mason D.Y.;
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Matches 598; Conservative 161; Mismatches
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Eur. J. Immunol. 23:2320-2325(1993)
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Pfam; PF00530; SRCR; 9.
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1116 AA; 120979 MW;
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EMBL, Y18394; CAB45233.1; JO
EMBL, Y18395; CAB45233.1; JO
EMBL, Y18395; CAB45233.1; JO
EMBL, Y18399; CAB45233.1; JO
EMBL, Y18399; CAB45233.1; JO
EMBL, Y18400; CAB45233.1; JO
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EMBL; Y18400; CAB45233.1; JO
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PS50287; SRCR_2;
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                     antigen precursor
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MEDLINE-93380506; PubMed-8370408;
Law S.A., Micklem K.J., Shaw J.M., Zhang X.P., Dong Y., Willis A.C.,
Mason D.Y.;
                                                                                 MEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAI
                                                                                                                                                     VNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRV
                                                                                                                                                                                                                                                                                                                               IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN
                                         SLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A new macrophage differentiation antigen which is a member of scavenger receptor superfamily.";
ELI. J. Immunol. 23:230-2325(1993).
EMBL: 222970; CAA80543.1;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
M130 antiqen cytoplasmic variant 2 precursor.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                         364 GADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAK 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 EWGTICDDGWDSYDAAVACKQLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 RNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      723 IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN
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                                                                                                                                                               M130 ANTIGEN CYTOPLASMIC VARIANT W; 3BEEC22D805B1D5C CRC64;
                                                                                                                                                                                                                         Length 1156;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                       Query Match 42.1%; Score 3429; DB 4; Best Local Similarity 56.2%; Pred. No. 3.8e-259; Matches 598; Conservative 161; Mismatches 294;
                                                                                                                                            POTENTIAL
InterPro; IPR001190; Srcr_receptor. Pfam; PF00530; SRCR; 9. PRINTS; PR00228; SPRACTRCPTR. SMART; SM00202; SR; 9. PROSITE; PS50287; SRCR_1; 4. PROSITE; PS50287; SRCR_2; 9.
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1156 AA; 125352 MW;
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IHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRCAGRV 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RISSPAEETWITCEDRIRVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGC 1289
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                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-21243729; PubMed-11345593;
Schaer D.J., Boretti F.S., Hongegger A., Poehler D., Linnscheid P.,
Staege H., Muller C., Schoedon G., Schaffner A.;
                                                                                                                                                                                                                                                                                                       -----YTDVRLVNGKSQCDGQVEINVLGHWGSLCDTHW
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                                                                    DPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGNESLLDNCQMTVLGAPPC
                                          IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN
                                                                                                                                MEASLICSAHROPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAI
                                                                                                                                                                                                                     SLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSR----
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Macrophage Hemoglobin scavenger receptor CD163 precursor.
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                                              HAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL
                                                                                                                              WDCHAKPWGQSDCGHKEDAGVRCSGQSLK - - - - SLNASSGHLALILSSIFGLLLLVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 PSNEARDIWINSISCTGNESALWDCTYDGKAKRT-CFRRSDAGVICSDKADLDLRLVGAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 40 POTENTIAL.
41 1149 M130 ANTIGEN EXTRACELLULAR VARIANT.
1149 AA; 124328 MW; FDBA6D85CF97BB60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'A new macrophage differentiation antigen which is a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 41.7%; Score 3396.5; DB 4; Length al Similarity 54.4%; Pred. No. 1.3e-256; 597; Conservative 161; Mismatches 295; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-93380506; PubMed-8370408;
Law S.A., Micklem K.J., Shaw J.M., Zhang X.P., Dong Y.,
Mason D.Y.,
                                                                                                                                                                                                                1377 I -- LFLTWCRVQKQKHLPLRVSTRRGSLEENLFHEMETCLKRED 1419
                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M130 antigen extracellular variant precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scavenger receptor superfamily.";
Eur. J. Immunol. 23:2220-2325(1993).
EMBL; 222971; CAA80544.1; -.
PICEPPO: IPRO01190; Srcr_receptor.
Pfam; PF00530; SRCR; 9.
PRINTS; PR00258; SPERACTRCPTR.
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PROSITE; PS00420; SRCR_1; 4.
PROSITE; PS50287; SRCR_2; 9.
                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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Matches
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Homo sapiens (Human).
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"Molecular cloning and characterization of the mouse CD163 homologue, a highly glucocorticoid-inducible member of the scavenger receptor crysteine-rich family."; Immunogenetics 53:170-177(2001).

EMBL: AF274883; AAK16065.1; -MGD; MGI:2135946; CG163.

InterPro; IPR001190; Srcr_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 CSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAKPSNEARDIWINSIS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 CSGRVELKIHDKWGTVCSNGWSMNEVSVVQQQLGCPTSIKALGWANSSAGSGYIWMDKVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 CIGNESALWDCTYDGKAKRICFRRSDAGVICSDKADLDLRLV-GAHSPCYGRLEVKYQGE 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSGWGKHNCVHREDVIVICSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKA 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 GSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICSDGADL--ELRLADGSNN 377
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120889 MW; 04428DF18AD26187 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Query Match . 40.2%; Score 3272; DB 11;
Best Local Similarity 52.4%; Pred. No. 6.9e-247;
Matches 582; Conservative 174; Mismatches 332;
                                                                                                                                                                                                                               PROSITE; PS00420; SRCR_1; UNKNOWN_3.
PROSITE; PS50287; SRCR_2; 9.
                                                                                                                                                                                    PRINTS; PR00258; SPERACTRCPTR. SMART; SM0202; SR; 9.
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                                                                                                                                                                                                                                                                                                                                         1334 DCGHKEDAGVRCSGQSLKSLNASSGHLALILSSIFGLLLLVLFILFLTWC----RVQKQK 1389
957
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Mollenhauer J., Holmskov U., Wiemann S., Krebs I., Herbertz S.,
Mollenhauer J., Kloschis P., Coy J.F., Poustka A.;
"The genomic structure of the DMBTI gene: evidence for a region with
susceptibility to genomic instability.";
Oncogene 18:6233-6240(1999).
I. Oncogene 18:6233-6240(1999).
I. SIMILARITY: COUTAINS 2 CUB DOMAINS.
REMBL; AJ243224; CAB63942.1; -
R InterPro; IPR0010507; EndGoglin/Ciolo5.
R InterPro; IPR001190; Srcr_receptor.
R Pfam; PF00431; CUB; 2.
R Pfam; PF00431; CuB; 2.
R PFINTS; PR00536; SRFRACTRCPTR.
R PRINTS; PR00258; SPERACTRCPTR.
R SMART; SM00201; SR: 14.
R SMART; SM00201; SR: 14.
                                                                                       RLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAPLSKTGSGFMWVDDIQCPK
                                                                                                                                            RLEVFYNGTWGSIGSSNMSPTTVGVVCRQLGCADNGTVKPIPSDKTPSRPMWVDRVQCPK
                                                                                                                                                                                                                                   898 GVDTLWQCPSSPWKQRQASPSSQESWIICDNKIRLQEGHTDCSGRVEIWHKGSWGTVCDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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IW; 902622DE7399AD38 CRC64;
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Last annotation update)
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PROSITE; PS010420; SRCR.1; UNKNOMN_13.
PROSITE; PS50287; SRCR.2; 14.
PROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
26 2403 DMBT1/8KB
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Query Match 36.7%; Sc Best Local Similarity 39.7%; Pr Matches 615; Conservative 181;	1307 DVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQPT-PSPDTWPTSHASTAGSE 1365 1026 SALICLEDKRLRLVDGDSRCAGRVEIXHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNA 1085	DP Qy
Signal. 1 25 SIGNAL 26 2426 CHAIN 26 2426 SEQUENCE 2426 AA; 262052	GDRCQGRVEVLYRGPWGTVCDDYWDTNDANVVCRQLGCGWATSAPGNARFGQGSGPIVLD RFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEG	o o
	970 HLALCPIVQHPEDTCIHSREVGVVCSRYTD	oy ob
	######################################	Oy Dp
DR InterPro; IPR001507; Endoglin/C DR InterPro; IPR001190; Srcr_recep DR Pfam; PF00431; CUB; 2.	774 WKQTACHLNMEASLICSAHR-QP	Qy Db
R. Oncogéne 18 6533 - 6940(1999). CC -1 - SIMILARITY: CONTAINS 2 CUB DR BEBLY, AZ423211; CAB63941.1 DR TherPro: IPR000859: CUB Gomain	714 LCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWE 773 :	QY Db
	678 VGVICSDASDMELRLVGGSSRCACKVEVNVQGAVGI 713	Oy Dp
Mannaid C. Tamacco. NCBL_TaxID=9606; [1] SEQUENCE FROM N.A. MFNT TAXE=20065089.	618 AVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSED 677	Qy dd
GN DMBT1. OS HOmo sapiens (Human). OC Bukaryota; Metazoa; Chordata; C	577GDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAA 617	Qy Dp
	520 GKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCS 576  1	Oy Ob
RESULT 8 Q9UGM3 DQ9UGM3 PRELIMINARY; PAC CONTINGS	470DKADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGC 519 :: 1	Qy Db
OY 1330 WGQSDCGHKEDAGVRCSGQSLKSLNA   :           :    Db 1714 WLTHNCGHHEDAGVICSATQINSTTT	424 PSNEARDIWINSISCTGNESALMOCTYDGKAKRTCFRRSDAGVICS	6
OY 1270 VCDDSWDLAEAEVVCQQLGGGSALAA		Oy d
	SGSSDVWLDGVSGGRESFLWDCRHSGTWFDCLHQNDVSVICS-D	8 8 8
Oy 1182 FQLGCGENGVVSLAPLSKTGSGF 	258SDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKNNNAADVVCKQLG 304 	Qy dd
	199 PSSFISSGVVNSPAVLRPIMLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDS-257 1	oy da
OY 1086 TVSAHEGEGSGPIWLDDLNCTGTESH	19	\$ G
Db 1366 \$SLALRLVNGGDRCQGRVEV	101 GQAVTRHGKIMLDDVSCYGNESALWECQHREWGSHNCYHGEDVGVNCYG 149 	O.y D

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22;
|: : | |||:||| || :||:|||| |: ||EVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWATSA 1419
                                    SHLWQCPSRGWGQHDCRHKEDAGVIC----- 1135
                                                                                        SEMWYDDIQCPKTHISIWQCLSAPW----- 1227
                                                                                                                                                             | : :||::|
GPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDA 1594
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Wiemann S., Krebs I., Herbertz S.,
.F., Poustka A.;
bMBTL gene: evidence for a region with
tability.";
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Pred. No. 3.3e-224;
; Mismatches 498; Indels 256; Gaps
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Catarrhin1; Hominidae; Homo.
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DMBT1 PROTOTYPE.
W; 5AS8FBC076FB7247 CRC64;
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	GTDLELRLVNGDGPCSGTVEVKFQGQWGTVCDDGWNTTASTVVCKQLGCPFSFAM	FREGAVTRHGKIWLDDVSCYGNESALWECQHREWGSHNCYHGEDVGVNCY	PESWPVRISPPVPTEGSESSLALELVDGNNSCSGRVEVEVKFQERWGTICDDGWNLNTAAVV		TCY	WNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVVMLDGVSCSGNESFLWDCRHSGTVNFD	CLHQNDVSVICS	HEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAKPSNEARDIWINSISCTGNESALW	DCTYDGKARRTCFRRSDAGVICSDKADLDLRLVGAHSPCYGRLEVK   ::	YQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGWTYFKEASGPIWLDDVSCIGNESNI  :	WDCEHSGWGKHNCVHREDVIVTCSGDATWGLRLVGG	SNRCSGRLEVYFGGRWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLD  :	DVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICS	DMELRLVGGSSRCAGKVEVNVQGAVGILCANGMGMNIAEVVCRQLECGSAIRVSREPHFT :	ERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLNMEASLICSAHRQ	PRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGD	AISLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSR	
	43	98 155	149	193	253	291 392	351 452	387	447 572	493	553 692	589 752	649	. 687	747	795	841	897
	δ G	ολ	9 Q	Qy Dp	9 P	ζo	QY Db	Qy	P G	\$ g	Sy Op	Oy Dp	Oy Dp	Q Dp	QY Dp	QY Dp	. 40	Qy Dp

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997 VICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGF 1056
                                                                                                          WGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCP 1116
                                                                                                                      1285 WGTVCDDYWDTNDANVVCRQLGCGWATSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCP 1344
                                                                                                                                                             1117 SRGWGQHDCRHKEDAGVICS------1152
                                                                                                                                                                                                                   1153 AGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAPLSK---TGSGFMWVDD 1209
                                                                                                                                                                                                                               1210 IQCPKTHISIWQCLSAPW------CEDR 1245
                                                                                                                                                                                                                                                                                        ::| :| | | | | 1460 VRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASGSOPTPSPDTWPTSRASTAGSEST 1519
                                                                                                                                                                                                                                                                                                                           1246 IRVR---GGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFG 1302
                                                                                                                                                                                                                                                                                                                                           937 LCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVS 996
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Tornoee I., Kliem A., Reid K.B., Poustka A., Skjoedt K.;
"Cloning of gp-340, a putative opsonin receptor for lung surfactant
protein D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                1303 QGTGTIWLDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKS 1352
                                                                                                                                                                                                                                                                                                                                                                                              1579 QGSGPIVLDDVRCSGHESYLMSCPHNGMLSHNCGHHEDAGVICSAAQSQS 1628
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
DMBT1/8kb.2 protein precursor.
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PROSITE; PS0420; SRCR 1; UNKNOWN_13.
PROSITE; PS0637; SRCR 2; 14.
PROSITE; PS06682; ZP_DOMAIN; UNKNOWN_1.
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TISSUE-TRACHEA;
MEDLINE=99415938; PubMed=10485905;
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SMART; SM00202; SR; 14.
SMART; SM00241; ZP; 1.
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PROSITE; Signal.
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	Gaps 22,	FRF 100 :  AQF 289	- 149 T 346	ic 198 	- 255 NH 466	29		41	46	IN 509 : 1D 766	RE 569     826	v 607     986	sw 667 1 sw 946	KV 703 :  RV 1006	SE 763     1066	rg 799 rn 1126	A 859 /L 1186 899
FT SIGNAL 1 25 POTENTIAL. FT CHAIN 26 2412 DMBT1/8KB.2 PROTEIN. SQ SEQUENCE 2412 AA; 260568 MW; 3F630CCBFFB18EDD CRC64;	Query Match 36.7%; Score 2987; DB 4; Length 2412; Best Local Similarity 40.1%; Pred. No. 3.5e-224; Matches 617; Conservative 177; Mismatches 506; Indels 240;	QY 44 TDLELRLVNGDGPCSGTVEVKFGGQWGTVCDDGWNTTASTVVCKQLGCPFSFAMFRF:	QY 101 GQAVTRHGKIMLDDVSCYGNESALWECQHREWGSHNCYHGEDVGVNCYG	OY 150EANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGC D::     :      :	OY 199 FSSFISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTCY DD 407 GWATSAPGNARFGGGSGPIVLDDVRCSGYESYLWSCPHNGMLSHNCQHSEDAGVICSAAH	256	Qy 295 AADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQ   1:111:1111   1   1   1   1   1   1   1	355		QY 470	OY 510 AAVVCKQLGGGKPMHVFGMTYFKEASGPIMLDDVSCIGNESNIWDCEHSGWGKHNCVHRE	QY 570 DVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTV	QY 608 CDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIMLDDVSCDGDESDLMSCRNSGW	QY 668 GNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKV :::	QY 704 EVNVQGAVGILCANGMGMNIAEVVCRQLEGGSAIRVSREPHFTERTLHILMSNSGCTGGE	QY 764 ASLWDCIRWEWKQTACHLNMEASLICSAHR-QP	OY 800 ADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLSVGDHFCKGNGLTWA  1127 GGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVACRQLGCGWAMSAPGNARFGQGSGPIVL  OY 860 EKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTD

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CDDYWDTNDANVVCRQLGCSWATSAPGNARF 1306
                                                                                                SAPPCIHGNTVSVICTGSLTQPLFPCLANVS 1015
                                                                                                                                                             CAGRVEIYHDGFWGTICDDGWDLSDAHVVCQ 1075
| |||||: | |||:||| || :||:||:
| CQGRVEVLYRGSWGTVCDDYWDTNDANVVCR 1419
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                                                                                                                  FSHNCGHHEDAGVICSASQSQPT-PSPDTWP 1365
                                                                                                                                                                                                                              LRLYSETETESCAGRLEVFYNGTWGSVGRRN 1171
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LRLVN--GGDRCRGRVEVLYQGSWGTVCDDY 1537
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                                UDTHWDPEDARVLCRQLSCGTALSTTGGKYI 955
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d) equence update) nnotation update) 2413 AA.

1 J., Vitved L., Gronlund J., stka A., Skjodt K.; onin receptor for lung surfactant lata; Vertebrata; Euteleostomi; rhini; Hominidae; Homo. )794-10799(1999). INS.

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SELALRLYNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWATSAPGNARF 1306
                                                                                                                                                                                                                                 DPYLSAVPEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQ 1075
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20017478; Pubmed-10551316;
Takeshita H., Sato M., Shiwaku H.O., Semba S., Sakurada A., Hoshi M.,
Hayashi Y., Tagawa Y., Ayabe H., Horii A.;
"Expression of the DMBTI gene is frequently suppressed in human lung
                                                                                                                                                                           DDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQPTPSPDTWPTSHASTAGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNE
                                                                            ----VRLVNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYI
                                                                                                                                                      GERSVRVWGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVS
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Catarrhini; Hominidae; Homo
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Last sequence update)
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  EXFQCEGSETHLALCPIVQHPEDICIHSREVGVVCSRYID-
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-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
EMBL; AB020812; BAA78577.1; JOINED.
EMBL; AB020813; BAA78577.1; JOINED.
EMBL; AB020814; BAA78577.1; JOINED.
EMBL; AB020814; BAA78577.1; JOINED.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE FROM N.A.
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AB020820;
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                                                                                                                                                                         TDLELRLVNGDGPCSGTVEVKFQGQWGTVCDDGWNTTASTVVCKQLGCPFSFAM---FRF 100
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                                                                                                                                  240;
                                                                                                Length 2413;
                                                                                                              Best Local Similarity 40.1%; Pred. No. 1.2e-223;
Matches 618; Conservative 177; Mismatches 505; Indels
PS00420; SRCR_1; UNKNOWN_13.
PS50287; SRCR_2, 14.
PS06687; ZP DDMAIN; UNKNOWN_1.
2413 AA; 260755 MW; 039544043CF463D4 CRC64;
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                                                                                          Score 2980; DB 4;
Pred. No. 1.2e-223;
                                                                                            36.6%;
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ABO20822; ABO20824; ABO20824; ABO20825; ABO20826; ABO20826; ABO20829; ABO20831; ABO20831; ABO20831; ABO20831; ABO20831;	AB020834 BAA78577.17 AB020835 BAA78577.17 AB020836 BAA78577.17 AB020837 BAA78577.17 AB020838 BAA78577.17 AB020839 BAA78577.17 AB020841 BAA78577.17 AB020842 BAA78577.17 AB020844 BAA78577.17 AB020844 BAA78577.17 AB020844 BAA78577.17 AB020844 BAA78577.17 AB020844 BAA78577.17 AB020844 BAA78577.17		Query Match  Best Local Similarity  30.1%; Score 2448; DB 4; Length 1785;  Best Local Similarity  36.2%; Pred. No. 3.2e-182;  Matches 534; Conservative 156; Mismatches 413; Indels 374; Gaps 28  43 GTDLELRLVNGDGPCSGTVEVKFOGGWGTVCDDGWNTTASTVVCKQLGCPFSFAM 97  1

oy d	351	VE.	
3	704	ov LCSAA	470
QY	411	GCPFSVFGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSD	470
Qy	471	KADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTY	m
QQ	492	LALRLVNGGDRCQGRVEVLYQGSWGTVCDDSWDTNDANVVCRQLGCGWAMSAPGNAR	548
QY	531	FKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDATW-	581
qq	549	FGQGSGPIVLDDVRCSGHESYLMSCPHNGWLSHNCGHSEDAGVICSASQSRPTPSPDTWP	608
δλ	582	GLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDCPS	628
QQ	609	TSHASTAGSESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGW	668
δλ	629	SIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICS	683
Dp	699	AMSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQ	728
δy	684		726
QQ	729	PTPSPDTWPTSHASTAGSESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANV	788
Qy	727	VCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLNMEAS	786
qq	789	VCRQLGCGWATSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAG	848
Qy	787	LICSAHR-QPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLS	845
Dp	849	VICSASQSQPTPSPDTWPTVICSASQSQP	867
Οy	846	VGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLVNG	905
pp	868	IIII	886
QY	906	KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGH	965
pp	887	GDRCRGRVEVLYQGSWGTVCDDYWDINDANVVCRQLGCGWAMSAPGNAQFGQGSGPIVLD	946
Οy	996	RFHCLGNESLLDNCOMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVP	102
qq	947	DVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSAAQSQSTPRPDTWLTTNLPALTVGS	100
Οy	1024	EGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAF	108
QQ	1007	ESSLALRLVNGGDRCRGRVEVLYRGSWGTVCDDSWDTNDANVVCRQLGCGWAM	105
Óλ	1084	NATVSAHFGEGSGPIMLDDLNCTGTESHLMQCPSRGWGQHDCRHKEDAGVICSEFTALRL	114
Dp	1060	SAPGNARFGGGSGPIVLDDVRCSGNESYLWSCPHKGWLTHNCGHHEDAGVICSATQI	111
Qγ	1144	YSETETESCAGRLEVFY-NGTWGS	116
QD	1117	NSTITDWWHPTTTTTARPSSNCGGFLFYASGTFSSPSYPAYYPNNAKCVWEIEVNSGY	117
δy	1167	VGRRNIAP	119
QQ	1175	RINLGFSNLKLEAHHNCSFDYVEIFDGSLNSSLLLGKICNDTRQIFTSSYNRMTIHFRSD	123
δy	1197	LSKTGSGFM-WVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGDTEC	125
qq	1235	ISFONTGFLAWYNRLVNLNSSYGLC	1267
Οÿ	1256	SGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRC	131
Db	1268	AGRVEIYHGGTWGTVCDDSWTIQEAEVVCRQLGCGRAVSALGNAYFGSGSGPITLDDVEC	1327

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946 SAPHSSFFGPGRGDILLDDVSCTGSEDDILDC---SHPPIGTNNCGHSEDAGVVCD--LN 1000
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                                                                                                                              552 IWDCEHSGWGKHNCVHREDVIVTCSGDATWG-----LRLVGGSNRCSGRLEVYFQGRWG
                                                                                                                                                   TVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNS
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01-NOV-1999 (TrEMBLrel. 12, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSCAYVSSHNCAHSEDAGVVCAGSGDGNIRLVGGSHSSEGRVELYVNNQWGTVCDDLWD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTASTVVCKQLGC-PFSFAMFRFGQAVTRHGKIWLDDVSCYGNESALWECQHREWGSHNC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPSSFISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSDIRVVGGRSPTEGRVEVFVNRAWGTVCDDLWDVNDTNVACRQLGFGRAISAPGGASY 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAKP ~ - SNEARDIWIN 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SISCTGNESALWDCTYDGKAKRTCFRRSDAGVIC -- - SDKADLDLRLVGAHSPCYGRLEV 491
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinocea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNDAQVACRQLGLGPAVSADAHFGEG --- SGSILLDNVACIGTETSLLSCSHPGIESHNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGRAISASGGASYGGGSGSIFLDNLACTGAESNLLSCPHNGVGSHNCGHGEDAGVLCSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97;
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                                                                                                                                             01-WAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Scavenger receptor cysteine-rich protein type 12 precursor.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99328904; PubMed-10398804; Bancer Z., Rast J.P., Davidson E.H.; Politins of immunity: transcription factors and homologues genes of the vertebrate immune system expressed in sea urch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.0%; Score 2439.5; DB 5; Length ilarity 38.2%; Pred. No. 1.9e-181; Conservative 197; Mismatches 560; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98C51996A272A010 CRC64;
                                                                                                                                                                                                                                                          Strongylocentrotus purpuratus (Purple sea urchin).
1316 KGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKS 1352
                      2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Imminogenetics 49:773-786(1999).
EMBL; AF064259; AAD08654.1;
Interpro; IPR001190; Srcr_receptor.
Pfam; PF00530; SRCR; 20.
PRINTS; PR00258; SPERACTRCPTR.
SMART; SM0202; SR; 20.
PROSITE; PS00420; SRCR.1; 15.
PROSITE; PS00420; SRCR.1; 15.
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2153 AA; 226557 MW;
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
2153
                                                                                                                                                                                                                                                                                                             Strongylocentrotus.
NCBI_TaxID=7668;
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527; Conserv
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Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 FRFGQAVTRHGKIWLDDVSCYGNESALWECQHREWGSHNCYHGEDVGVNCY----- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 CRQLGCPSSFISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 WNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCPFSVFGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSD 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 GTD--LELRLVNGDGPCSGTVEVKFQGQWGTVCDDGWNTTASTVVCKQLGCPFSFAM--- 97
                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 25 POTENTIAL.
26 1785 DMBT1/6KB.1 PROTEIN.
1785 AA; 193941 MW; 7B1F8D47E4A82092 CRC64;
(TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.9%; Score 2435; DB 4; Best Local Similarity 36.1%; Pred. No. 3.3e-181; Matches 533; Conservative 155; Mismatches 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - LSMSH - - -
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-----PSPDTLPTITLPASTVGSESS---
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PROSITE; PS0420; SRCR_1; UNKNOWN_8.
PROSITE; PS050287; SRCR_2; 9.
PROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00258; SPERGTRCPTR.
SMART; SM00042; CUB; 2.
SMART; SM00202; SR; 9.
SMART; SM00241; ZP; 1.
PROSTUR.
                                                    DMBT1/6kb.1 protein precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fam; PF00431; CUB; 2.
fam; PF00530; SRCR; 9
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
01-NOV-1999
01-JUN-2002
                                                                                                                                                                                                                                                                          TISSUE=LUNG
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QY	471	KADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTY 530
ΟŸ	531	FKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDATW- 581
Ob	549	PSPD
Qy	582	GLRLVGGSNRCSGRLEVYFOGRWGTVCDDGWNSKAAAVVCSQLDCPS 62
qq	609	9 M
QY	629	68
qq	699	AMSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQ 728
Qy	684	
qq	729	PIPSPDIWPISHASTAGSESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDYWDINDANV 788
οy	727	VCRQLECGSAIRVSREPHFTERTLHILMSNGCTGGEASLWDCIRWEWKQTACHLNMEAS 786
qa .	7'89	VCRQLGCGWATSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAG 848
QY	787	LICSAHR-QPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLS 845
qq	849	VICSASOSOP
Qy	846	CPIVQHPEDTCIHSREVGVVCSRYTDVRLVN
qa	898	SRASTAGSESTLALRIVIG 886
Qy	906	KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSFTGGKYIGERSVRVWGH 965
qa	887	GDRCRGRVEVLYQGSWGTVCDDYWDTNDANVVCRQLGCGWAMSAPGNAQFGQGSGPIVLD 946
Qy	996	RFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQ-PLFPCLANVSDPYLSAVP 1023
qg .	947	DVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSAAQSQSTPRPDTWLTTNLPALTVGS 1006
Qy	1024	EGSALICLEDKRIRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAF 1083
QC	1001	ESSLALRLVNGGDRCRGRVEVLYRGSWGTVCDDSWDTNDANVVCRQLGCGWAM 1059
Qy	1084	NATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTALR1 1143
QQ	1060	SAPGNARFGGGSGPIVLDDVRCSGNESYLWSCPHKGWLTHNCGHHEDAGVICSATQI 1116
QY	1144	YSETETESCAGRIEVEY-NGTWGS
qq	1117	SUCGGELFYASGTFSSPSYPAYYPNNAKCVWEIEVN
QY	1167	TTAIAGIVCROLGCGENGVVSL
qq	1175	RINLGFSNLKLEAHHNCSFDYVEIFDGSLNSSLLLGKICNDTRQIFTSSYNRWTIHFRSD 1234
QY	1197	WERRISSPAEETWITCEDRIRVRGGI
qQ .	1235	ISPQNTGFLAWYNREPSPATERLVNLNSYGLC 1267
QY	1256	SGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGGGTGTIWLDDMRC 1315
qu	1268	AGRVEIYHGGTWGTVCDDSWTIQEAEVVCRQLGCGRAVSALGNAYFGSGSGPITLDDVEC 1327
Qy	1316	KGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKS 1352
අු	1328	SGTESTLWQCRNRGWFSHNCNHREDAGVICSGNHLST 1364
RES 096 ID	RESULT 15 096943 ID 09694	3 PRELIMINARY; PRT; 2043 AA.

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630 YDANVVCRQLGYDGAYNATHSSYYGDSGLTTVTAYTDCFGQESQLANCTGFRYPPYIPSW
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                                                                                                           Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Astrophorida; Geodiidae; Geodia.
NCBI_TaxID=6047;
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** MEDLINE-98369060; PubMed-9701562;

** Blumbach B., Pancer Z., Diehl-Selfert B., Steffen R., Mus Mueller I., Mueller W.E.G.;

** Mueller I., Mueller W.E.G.;

** The putative sponge aggregation receptor: Isolation and characterisation of a molecule composed of scavenger recognizer. The putative sponge aggregation receptor: Isolation and characterisation of a molecule composed of scavenger recognerated and special scalinities. The Special Scalinities. Scaring R. P. Coll Sci. 111:2635-2644(1998).

** RMBL; Y14953; CAA75175.1; Therefore IPR00139; Str. receptor.

** InterPro: IPR000136; Sushi_SCR_CCP.**

** RP Pfam; PR00084; Sushi_SCR_CCP.**

** RP RINTS; PR00084; Sushi_SCR_CCP.**

** RP RINTS; SM00032; CCP; 6.**

** RMRT; SM00032; CCP; 6.*
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            AY-1999 (TrEMBLrel. 10, Created)
AY-1999 (TrEMBLrel. 10, Last sequence update)
AR-2002 (TrEMBLrel. 20, Last annotation update)
domain, membrane form 2.
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PROSITE; PS50287; SRCR_2; 14.
SEQUENCE 2043 AA; 220896 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 32.4%; Pries 514; Conservative 196;
                                                                                                  Geodia cydonium (Sponge)
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                                                                                                                                                                                                                                                                                                                               574 TCSG-----DATWGLRLVGGS----NRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLD
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-----SDKADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVC
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Job time : 71 secs

## GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd

May 12, 2003, 02:36:30 ; Search time 7768 Seconds ' OM nucleic - nucleic search, using sw model Run on:

(without alignments) 17338.798 Million cell updates/sec US-09-759-130B-379 4628

1 geggeegetegegatetaga.....aaaeggaegegégégégégee 4628 Title: Perfect score: Sequence:

77. - 3.-- 1. 2054640 segs, 14551402878 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmb1:\*

Database

em\_htg\_other em\_htg\_mus:\* fun: еш\_го:\* b\_sts: em\_om: =m\_or: em\_pat em\_sts : un-a : mu\_me em\_ov : gb\_pl: gb\_pr:

Pred. No. is the number of results predicted by chance to have a

em\_htgo\_mus:\* em\_htgo\_other:\*

em\_htgo\_hum:\*

em\_htg\_rod:\* em\_htg\_vrt:\*

score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

## SUMMARIES

_	. +[ 1300		<b>90</b>			SUMMARIES	The state of the s
-	NO.	Score	Match	Length	DB	ID	Description
		რ.0	98.	4579	σ v	AF264014	264014 Homo's
	4 m	24.09	4.4	2249	0 0	58038	AXISSES: Sequence AXOSBO38 Homo sant
	4	450.	31.	3786	6	130AC1	Z22969 H.sapiens m
	ı,	448	31.	4950	σ (	30AC2	222970 H. sapitens m
	م ۵	448 409	4 30.5	3707	n vo	50A 1768	AX2811768 SectionSec
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	σ,	270.	27.	4405	10	383	AF274883 Mus muscu
	10	9.0	6 5	2205	<b>♂</b> ▼	AR F	X63723 B. bovis WCI
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	c 13	17.	11.	202252	7	7.	AC131207 Home Sapi
	14	. 9	10.	2165	4 -	22	AF400122 Ovisi Arie
	16	24.	. 6	7006	<del>4</del> M	6.	APOS4259 Strongello
	17	85.	ω.		4		x99335 S. scraff mR
	18	62.	۲.	177768	7	90	AC131206 Homo sapi
	20	າເ		3431	# M	26	AR228826 Strongvlo
	21		7.	2	4		X99336 IS. scroft mR
	22	0	7	202252	7	70	AG131207 Homo Aapı
	23	m o	0	7656	σ ο	224	AJ24324 Homo sapi
	25		6	7667	ת ס	335	A1297935 Homo sapi
	56		9	7683	6	212	AJ243212 Homo sapi
	. 27	56	.5	6323	ო .	53	Y14953 Geodia cydo
	78 78			3187	4 v	0	X99332 S.scrota mR ABO51832 Gallus da
	30	24.	4	5695	9	397	Y18397 Homo sapien
	31	96	4.	461	9	93	AX237293 Sequence
	3.5	. 6	4. <	5802	ی م		A90822 Sequence 1
	34	97.	. 4	5802	9 0		AJ000342 Homo sapi
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	36	97.	4.	3350	φ =		A83630 Sequence 1
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	39	94.	4	٥	m	F076513	AF076513 Strongylo
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	7 7	, 5 , 5	. 4	2356	א ע	3823	AF228823 SCTONGY10 A83632 Semence:3
	44	92.	4	2356	10	MMY13192	Y13192 Mus musculu
	45	90.	4	538	4	0118	AF400118 Ovis arie
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-,	SOURCE	;	sapi	5			
	ORGANISM		Homo sapie Eukaryota;	ens Metaz	oa;	Chordata; Craniata; Ver	tebrata; Euteleostom1;

REFERENCE AUTHORS TITLE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4579) Gronlund,J., Vitved,L., Lausen,M., Skjodt,K. and Holmskov,U. Cloning of a novel scavenger receptor cysteine-rich type I

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DCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWGCRNSGWGNNDCSHSEDVGVIC
SDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQLECGSAIRVS
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GADWPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLSVGDHFGKGNGL
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ESFLWDCRHSGTVNFDCLHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWT
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'LTWCRVQKQKHLPLRVSTRRRGSLEENLFHEMETCLKREDPHGTRTSDDTPNHGCED
'SDTSLLGVLPASEATK"
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                                                                                                                   droehlund, U., Vitved, L., Lausen, M., Skjodt, K. and Holmskov, U. Direct Submission Submitted (05-MAY-2000) Department of Immunology & Microbiology, Institute of Madical Biology, University of Southern Denmark, Odense University, Minsloewparken 21.1, Odense 5000, Denmark Location/Qualifiers
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'note="Region: scavenger receptor cysteine-rich domain
'RCR 3"
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transmembrane molecule (M160) expressed by human macrophages.
J. Immunol. 165 (11), 6406-6415 (2000)
20540099
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/product="scavenger receptor
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/note="Region: s
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/note="Region: scavenger receptor cysteine-rich domain
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/note="Region: connecting peptide"
4094. .4771
/note="Region: transmembrane domain"
4172. .4384
                                                            interdomain segment"
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Matches 4550; Conservative C
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	CTGAGGCT	GGTGGG	GTAGCCAGCTGGACTGCCCAT 	GAAAAAT            GAAAAAT	GGAACAG	TGAT	TTGAGGT           TTGAGGT	TIGCIGA           TIGCIGA	CTCATTI 	AAGCCTC	TGGAAGO 	CCTGCTC	ATTTCTC	CTCTTTC	AGTGTGP 	CTTGTAT	ACTTGTGAATGGCAAATCCCAGTGTGACGGGCAAGT 	CACTGTG
	0000	CAAGGAC                     CAAGGAC	TGTAGCC  + - -  TGTAGCC	GGATATG             GGATATG	ICTCTGGTCATGCAGGAACAGTGGGTGGGGAATAATGACTV 	TGTT	GGAAAAG             GGAAAAG	CTGGGGAATGAACATTGCTGAAGTTGTTTGCAGGCAACTTGAATGTGGGTGTGCAATCAG 	AGAGAGC          AGAGAGC	GGAGGGG 	TTAAATA          TTAAATA	GATATGC         GATATGC	GATTCTG             GATTCTG	GCCATAT           GCCATAT	AAGTTCC             AAGTTCC	GAAGACA          GAAGACA		GGACACTGGGGCTCACTGTGACACCCACTGGGACCCAGAAGATGCCCGTG
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rrg 67	SCAGACATCGTGG 7	AGTAG 8         AGTAG 7	CTGAA 86        CTGAA 85	GATGT 92          GATGT 91	TTGCA 98	TTTCT 104	Grerc 110	AATTG 116	3 122	rrrgG 128        rrrgG 127	3 134 	3 140   3 139	14	4 4	GTAAACAATGGG 158 GTAAACAATGGG 158	CCTAT 164	CACAG 170	SGIGA 17
GCTGTATTGCGCCCCATTTG 67	SAATTGCAGACATCSTGG 7 	AGTAG 8         AGTAG 7	GGGAGAGTAGAGCTGAA 86 	GATGT 92          GATGT 91	TTGCA 98	TTTCT 104	Grerc 110	AATTG 116	3 122	rrrgG 128        rrrgG 127	3 134 	3 140   3 139	14	4 4	GTAAACAATGGG 158 GTAAACAATGGG 158	CCTAT 164	CACAG 170	SGIGA 17
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GOONCRHKEDAGVICSEFMSIRLTSEASREACAGRLEVFYNGAWGTVGKSSMSEFTVG
VYCRQLGCADKGKINPASLDKAMSIPWWYDNVQCPKGPDTLWQCPSSPWEKRLASPSE
                                                                                                                                                                                                                                                ETWITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQVVCQQLGCGPALK
AFKEAEFGQGTGPIWLNEVKCKGNESSLWDCPARRWGHSECGHKEDAAVNCTDIŞVQK
                                                                                                                                                                                                                                                                                              TPQKATTGESSROSSEIAVGILGVVLLAIEVALFELTKKRRORORLAVSSRGENLVHQ
IOYREMNSCLNADDLDLANSSENSHESADFSAAELISVSKFLPISGMEKEAILGHTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps. 3;
PAVWOCKHHEWGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRLLGKV
                                              QWGGLTCDHYEEAKITCSAHREPRLVGGDIPCSGRVEVKHGDTWGSICDSDFSBEAAS
                                                                                               DVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKGGVA
                                                                                                                    LSTPGGAREGKGNGQIWRHWFHCTGTEQHMGDCPVTALGASLCPSEQVASVICSGNQS
                                                                                                                                                QTLSSCNSSSLGPTRPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
                                                                                                                                                                       DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCNGKESRIWQCHSHGW
                                                                     VLCRELOCGTVVSILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSHSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1302 TAATGAAGCTAGAGACATTTGGATAAACAGCATATCTTGCACTGGGAATGAGTCAGCTCT
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Pred. No. 0;
0; Mismatches 1129;
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/evidence=experimental
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Best Local Similarity 65.4%;
Matches 2182; Conservative
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pp Ωp qq qq ò qq δ q δ QQ δy Q δy g Óλ g οy Q ò рp Q q δ g οχ οy q οy ò g ò g ōλ qq ò ò οy 1718 1778 1838 1898 2018 2138 2198 2318 2378 2438 2498 1606 2558 1666 2618 1726 2678 886 TTCTGTGGGAGATCACTTTGGAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCAGTG CTGGGGGGGGGCTCACTTGGAGGGAATGGACAGATCTGGCTGAGAATTCCAGTG TTGTGTACACAGAGGATGTGATTGTAACCTGCTCAGGTGATGCAACATGGGGCCTGAG AATTTGGCTCGATGATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAA GGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGTGTATGCTGGGGGGGAATGAACATTGC AGCAAGTTTGATCTGCTCAGCCCACAGGCAGGCTGGTTGGAGGTGATATGCCCTG GCTGGTGGCGCGCAGCAACCGCTGGCAAGACTGGAGGTGTACTTTCAAGGACGGTG GGACTGCCCATCTTCTATCATTGGCATGGGTCTGGGAAACGCTTCTACAGGATATGGAAA CAGTGGGTGGGGAAATAATGACTGCAGTCACAGTGAAGATGTTGGAGTGATCTGTTCTGA TGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCAGAGAGCCTCA TTTCACAGAAAGAACATTACACATTTAATGTCGAATTCTGGCTGCACTGGAGGGGAAGC 1659 1187 2379 2559 767 1719 827 1779 887 1839 947 1899 1001 1959 1067 2019 1127 2079 2139 1247 2199 1307 2259 1367 2319 1427 1487 2439 1547 2499 1607 1667 2619 1727 1787 ò q QY Db ò g δ g ò g ò g o g ογ ద S a 9 9 9 9 g õ q ò g S 셤 ò g ò g õ a õ q

2798 1.956 2146 2206 3218 3518 2686 1906 2026 2978 2086 3158 22,66 2326 2386 3338 2446 3398 3458 2566 2626 3578 3638 3698 2806 3038 2506 3818 CTGTAACTCTCACTGGGACATAGAAGATGCCCATGTTCTTTGCCAGCAGCTTAAATGTGG AGAAAGTGCTGTGGCTGCATAGAGAGTGGTCAACTTCGCCTGGTAAATGGAGGAGGTCG CATGTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCTCCATATGGCAGTGCCTGTC FILLIFICATION FOR THE FORM OF CAAGATAAGACTTCAGGAAGGACCCACTTCCTGTTCTGGACGTGTGGAGATCTGGCATGG AGGCTCCTGGGGCACAGTGTGTGATGACTCCTGGGACCTGGCCGAGGCGGAAGTGGTGTG TGGCAAATCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCTTGGACACTGGGGCTCACT GTGTGACACCCACTGGGACCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAGCTGTGG GACTGCTCTCTCAACCACAGGAGGAAAATATATTGGAGAAAAAAGAAGTGTTCGTGTGTGGGG ACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCT CCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTTGTCTGCAGTTCCAGA GGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGATGGGGACAGCCG CTGTGCCGGGAGAGAAGATCTATCACGACGCTTCTGGGGCCACCATCTGTGACGG ATGCAATGGAAAAGAATCCCGCATTTGGCAGTGCCATTCACACGGCTGGGGGCAGCAAAA CTGCAGGCACAAAGAGGACGCAGGGGTCATCTGCTCAGAATTCACAGCCTTGAGGCTCTA CAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGAAGTCTTCTATAACGGGACCTG GGGCTGTGGGGGAGATGGAGTTGTCAGCCTCGCCCTTTATCTAAGACAGGCTCTGGTTT TGCCCCATGGGAGCGAAGAATCTCCAGCCCAGCAGAAGAGACCTGGATCACATGTGAAGA TAGAATAAGAGTGCGTGGAGGAGACACCGAGTGCTCTGGGAGAGTGGAGATCTGGCACGC 2919 3219 3279 2447 3819 2739 1847 2799 2859 2027 2979 2087 2147 3099 2207 3159 2267 2327 2387 3339 3399 2507 3459 2567 3519. 2627 3579 2687 2747 3699 1907 1961 3639 2807 2867

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PRI 22-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submission Submitted (14-JUN-1993) Kingsley K.J. Micklem, Nuffield Department Submitted (14-JUN-1993) Kingsley K.J. Micklem, Nuffield Department Radcliffe, Hospital, Headington, Oxford, Ox3 9DV, United Kingdom 2 (bases 1 to 4950)
Law,S.K., Micklem,K.J., Shaw,J.M., Zhang,X.P., Dong,Y., Willis,A.C.
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                      CTGTCACGCCAAACCCTGGGGACAGAGTGACTGTGGACACAAGGAAGATGCTGGCGTGAG
                                                                                                                                                                                                                                                                                      TCATTTAGCACTTATTTTATCCAGTATCTTTGGGGCTCCTTCTCCTGGTTCTGTTTATTCT
                                                                                                                                                                                                                                                                                                                                             ATTICICACGIGGCCGAGITCAGAAACAAAACAICTGCCCCCTCAGAGITICAACCAG
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H.sapiens mRNA for M130 antigen cytoplasmic variant 2.
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Eur. J. Immunol. 23 (9), 2320-2325 (1993)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Macrophage"
102. .3572
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Mammalla; Eutheria; Primates;
1 (bases 1 to 4950)
Micklem,K.K.
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antigen; antigen M130.
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Homo sapiens
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RFQGEWGTICDDGWDSYDAAVACKOLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHE
PAVWQCKHHEWGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEJQRLJLGKV
                                                                                                                                                                                              QTLSSCNSSSLGPTRPTIPESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCNGKESRIWQCHSHGW
GQQNCRHKEDAGVICSEFWSLRLTSEASREACAGRLEVFYNGAWGTVGKSSMSETTVG
                                                                                                                                                                                                                                                            VVČRQLGCADKGK I NPASLDKAMS I PMWVDNVOCPKGPDT LWOCPSSPWEKRLASPSE
ETWITCDNK I RLQEGPTSCSGRVE I WHGGSWGTVCDDSWDLDDAQVVCQQLGCGPALK
AFKEAEFGQGTGP I WLNEVKCKGNESSLWDCPARRWGHSECGHKEDAAVNCTDISVQK
                                                                                                                                                                                                                                                                                                                            FPQKATTGRSSRQSSFIAVGILGVVLLAIFVALFFLTKKRRORORLAVSSRGENLVHQ
LQYREMNSCLNADDLDLMNSSGLWVLGGSIAQGFRSVAAVEAQTFYFDKQLKKSKNVI
                      DDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKGADLSLRLVDGVT|BCSGRLEV
                                                                                       CDRGWGLKEADVVCROLGCGSALKTSYQVYSKIQATNTWLFLSSCNGNETSLWDCKNW
                                                                                                       2WGGLTCDHYEEAKITCSAHREPRLVGGDIPCSGRVEVKHGDTWGSICDSDFSLEAAS
                                                                                                                                VLCRELOCGTVVSILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSHSR
                                                                                                                                                       DVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAMGSLCNSHWDIEDAHVL,CQQL,KCGVA
                                                                                                                                                                         LSTPGGARFGKGNGQIWRHMFHCTGTEQHMGDCPVTALGASLCPSEQVAS/VICSGNQS
NMCSGRIEIKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 AGACAAGGAGCTGAGGCTAGTGGATGGTGAAAACAAGTGTAGCGGGAGAGTGGAAGTGAA
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Pred. No. 0;
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'evidence=experimental
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65.4%;
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Matches 2178; Conservative
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mat_peptide
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ą	647	CTTCAACATAGATCATGTCTGTCATTTGTAGACAACTTGAATGTGGAAGTGCTGTCAG 706	
ž g	.1599	TGTGTTTGGTATGACCTATTTTAAAGAAGCATCAGGACCTATTTGGCTGGATGACGTTTC 1658 	
× 4	1659 767	TTGCATTGGAAATGAGTCAAATATCTGGGACTGTGAACACAGTGGGTGG	•
ž 4	1719 827	TTGTGTACACAGAGGATGTGATTGTAACCTGCTCAGGTGATGCAACATGGGGCCTGAG 1778	
λ q	1779 887	GCTGGTGGGCGCAGCAACCGCTGCTGGAAGACTGGAGGTGTACTTTCAAGGACGGTG 1838 	
<del>,</del> α	1839	GGGCACAGTGTGTGATGACGGCTGGAACAGTAAAGCTGCAGCTGTGGTGTGAGCCAGCT 1898 	
<u> </u>	1899	GGACTGCCCATCTTCTATCATTGGCATGGGTCTGGGAAACGCTTCTACAGGATATGGAAA 1958 	
<u>۲</u> و	1959 1067	AATTTGGCTCGATGATGTTTCCTGTGATGGAGTGAGTCAGATCTCTGGTCATGCAGGA 2018 	
સ્ટ જ	2019	CAGTGGGTGGGGAAATAATGACTGCAGTCACAGTGAAGATGTTGGAGTGATCTGTTCTGA 2078 	
č q	2079	TGCATCGGATATGGAGCTGAGGCTTGTGGGTGGAGCAGGGTGTGCTGGAAAAGTTGA 2138 	
ž a	2139	GGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAATGGCTGGGGAATGAACATTGC 2198 	
ž q	2199	TGAAGTIGTITGCAGGCAACTIGAATGTGGGTCTGCAATCAGGGTCTCCAGAGAGCCTCA 2258 	
දු පු	2259	TTTCACAGAAAGAACATTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGGAAGC 2318	
λ c q	2319	CTCTCTGGGGTTGTATÀCGATGGGAGTGGAACAGACTGCGTGTCATTTAAATATGGA 2378 	
දු පු	2379	AGCAAGTTTGAICTGCTCAGCCCACAGGCAGCCCAGGCTGGTGGAGCTGATATGCCCTG 2438	
ζ, G	2439	CTCTGGACGTGTTGAAGTGAAACATGCAGACATGGCGCTCTGTCTG	
ς G	2499	CTCTCTTCATGCTGCCAATGCTGTGGGAATTAAATTGTGGGAGTGCCATATCTT 2558 	
9 9	2559 1667	TTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCAGTG 2618 	
oy Op	2619 1727	TGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAACATCCGGAAGACACTTG 2678 	

2858 2978 2086 2,146 3158 2266 13278 2386 2446 3518 3578 2686 2738 2798 1966 2026 3038 3098 2326 3398 2506 3458 2566 2806 2866 CTGGGACCTGAGTGATGCCCACGTGGTTTGCAGACAGCTGGGCTGTGGAGAGGCCATTAA CTGCAGGCACAAGGAGGACGCAGGGGTCATCTGCTCAGAATTCACAGCCTTGAGGCTCTA CAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGTTGGAAGTCTTCTATAACGGGACCTG GGGCTGTGGGGAGAATGGAGTTGTCAGCCTCGCCCTTTATCTAAGACAGGCTCTGGTTT CATGTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCTCCATATGGCAGTGCCTGTC TATCCACAGCAGAGGTTGGAGTTGTCTGTTCCCGATATACAGATGTCCGACTTGTGAA ACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCT TGGAGCACCTCCCTGTATCCATGGAAATACTGTCTCTGTGATCTGCACAGGAAGCCTGAC CTGGGACCTGAGCGATGCCCACGTGGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTCAA CTGCACAGGAACGGAGTCCCACTTGTGCCAGTGCCCTTCCCGCGCGGCTGGGGCCACCAA TGGCAAATCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCTTGGACACTGGGGCTCACT CCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTTGTCTGCAGTTCCAGA 2979 2327 2387 2447 3399 2507 3519 3639 2679 1787 1967 2087 3039 3099 2207 3159 2267 3219 3279 3339 3459 2567 3579 2687 2747 2807 2739 1847 2799 1907 2859 2919 2027 2147 2627 g QQ οy ΩD οy a ò q qq QQ g δ g Š QQ δ qq δ qq ò g ò oy og ò QQ δ Ob ò QQ οy õ qq δ ö οy

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PRI 22-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n, Nuffield Department
Maternity Block, John
9DU, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A new macrophage differentiation antigen which is a member of the
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3759 TAGAATAAGAGTGCGTGGAGGAGACACCGAGTGCTCTGGGAGAGTGGAGATCTGGCACGC 3818
                              2926
                                                             3878
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                                                                                                                                                                                                                                                3999 CTGTCACGCCAAACCCTGGGGACACACGTGTGGACACACAAGGAGATGCTGGCGTGAG 4058
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                                                                                                                         TCAGCAGCTGGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTTGGCCAGGG
                                                                           2987 TCAACAACTIGGCIGIGCICCAGCITIGAAAGCAITCAAAGAAGCAGAGITIGGICAGGG
                                                                                                                                                                                      AACTGGAACCATCTGGTTGGATGACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGA
                                                             AGCCTCCTGGGGCACAGTGTGTGATGACTCCTGGGACCTGGCCGGAGGCGGAAGTGGTGTG
                                                                                                                                                                                                                                                                                                               4059 GTGCTCTGGACAGTCGCTGAA------ATCACTGAATGCCTCATGGG
                                                                                                                                                                                                                                                                                                                                           3167 TTGCACAGATATTTCAGTGCAGAAAACCCCACAAAAAGCCACAACAGGTCGCTCATCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAGGGTTCTCCGAGGAGAATTTATTCCATGAGATGGAGACCTGCCTCAAGAGAG
                             2867 CAAGATAAGACTICAGGAAGGACCCACTICCTGTTCTGGACGTGTGGAGATCTGGCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; E
Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-JUN-1993) Kingsley K.J. Micklem of Pathology, University of Oxford, Level 1, Radcliffe, Hospital, Headington, Oxford, OX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA.
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Eur. J. Immunol. 23 (9), 2320-2325 (1993)
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1. 3703
Arganism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="Macrophage"
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antigen.
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Mammalia; Eutheria; Primates;
1 (bases 1 to 3703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. sapiens mRNA for M130
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Micklem, K.K.
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Z22968.1
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VERSION
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PUBMED
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SOURCE
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/translation="MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDK
ELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAVSVICNOLGCPTAIKAPGWANSS
                                                                                                NMCSGRIEIKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWF
                                                                                                                          DDLICNGNESALWNCKHOGWGKHNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEV
                                                                                                                                                   RFQGEWGT ICDDGWDSYDAAVACKQLGCPTAVTA IGRVNASKGFGH IWLDSVSCQGHE
                                                                                                                                                                        PAVWQCKHHEWGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVE<sup>†</sup>1QRLLGKV
                                                                                                                                                                                                    CDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWLFLSSCNGNETSLWDCKNW
                                                                                                                                                                                                                        QWGGLTCDHYEEAKITCSAHREPRLVGGDIPCSGRVEVKHGDTWGSICDSDESLEAAS
                                                                                                                                                                                                                                                  VLCRELQCGTVVSILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSHSR
                                                                                                                                                                                                                                                                         DVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVA
                                                                                                                                                                                                                                                                                                  LSTPGGARFGKGNGQIWRHMFHCTGTEQHMGDCPVTALGASLCPSEQVASVICSGNQS
                                                                                                                                                                                                                                                                                                                      QTLSSCNSSSLGPTRPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEWKCNGKESRIWQCHSHGW
                                                                                                                                                                                                                                                                                                                                                                       GQONCRHKEDAGVICSEFMSLRLTSEASREACAGRLEVFYNGAWGTVGKSSMSETTVG
VVCRQLGCADKGKINPASLDKAMSIPMWYDNVQCPKGPDTLWQCPSSPWEKRLASPSE
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                                                                       AGSGRIWMDHVSCRGNESALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFKEAEFGQGTGPIWLNEVKCKGNESSLWDCPARRWGHSECGHKEDAAVNCTDTSVQK
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oy Op	2138	AGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAATGGCTGGGGAATGAACATTG 2197 	
Oy Dp	2198	CTGAAGTTGTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCAGAGAGCCTC 2257 	
oy Dp	2258	ATTICACAGAAAGAACATTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGAAG 2317 	
oy Op	2318	CCTCTCTCTGGGATTGTATACGATGGGAGTGGAACAGACTGCGTGTCATTTAAATATGG 2377 	
Qy Dp	2378	AAGCAAGTITGAICIGCICAGCCCACAGGGGCCCAGGCIGGGGGGGGGG	
Qy Dp	2436	CTGCTCTGGACGTGTTGAAGTGAAACATGCAGACACATGGCGCTCTGTGTGTG	
Qy Dp	2496	THICTCTCTTCATGCTGCCAATGTGCTGCAGAGAATTAAATTGTGGGGATGCCATATC 2555 	•
Qy Dp	2556 1667	TCTTTCTGTGGGAGATCACTTTGGAAAGGGAATGGTCTAACTTGGGCCGAAAAGGTCCA 2615 	
Oy Dp	2616 1727	GTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAACATCCGGAAGACAC 2675 	
0y Db	2676 1787	TTGTATCCACAGCAGAAAGTTGGAGTTGTCTGTTCCCGATATACAGATGTCCGACTTGT 2735 	
oy Op	2736 1847	GAATGGCAAATCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCTTGGACACTGGGGCTC 2795 	
oy Op	2796	ACTGTGTGACCCCCTGGGACCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAGCTG 2855 	
Oy Op	2856 1967	TGGGACTGCTCTCAACCACAGGAGAAAATATAGGAGAAAGAGTGTTCGTGTGG 2915 	
Oy Db	2916	GGGACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGT 2975 	
Oy Dp	2976 2087	TCTTGGAGCACCTCCCTGTATCCATGGAAATACTGTCTGT	
Oy Op	3036	GACCCAGCCACTGTTCCATGCCTCGCAAATGTATCTGACCCATATTGTCTGCAGTTCC 3095	
Oy Op	3096	AGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGATGGGGACAG 3155 	
δλ	3156	CCGCTGTGCCGGGAGGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGA 3215	

4216 3335 4.276 3275 2386 2446 2506 3455 2566 3515 2626 2686 3635 2,746 3694 5806 3754 3814 2926 3934 3106 4054 4096 3226 4156 1267 iCGCTGTGCTGGGAGAGTAGAGATCTATCATGAGGGCTCCTGGGGGACCATCTGTGATGA 2326 GAACTGCACAGGAACGGAGTCCCACTTGTGCCAGTGCCCTTCCCGCGGGCTGGGGGGCAGCA (3395) CTGGGGCAGCGTCGGCAGGAGGAACATCACCACAGCCATAGCAGGCATTGTGTGCAGGCA (3575 AGGGAACTGGAACCATCTGGTTGGATGACGTGCGGTGCAAAGGAAATGAGTCATTCTAT 3994 3107 GGGATTGTCCTGCCAGACGCTGGGGCCATAGTGAGTGTGGGCACAAGGAACACGCTGCAG 3166 GACCAGTGAAGCCAGAGAGAGGCCTGTGCAGGCGCTCTGGAAGTTTTTTACAATGGAGC 3456 CTACAGTGAAACTGAAACAGAGCTGTGCTGGGAGATTGGAAGTCTTCTATAACGGGAC GCTGGGCTGTGGGGAGAATGGAGTTGTCAGCCTCGCCCCTTTATCTAAGACAGGCTCTGG TTTCATGTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCTCCATAT-GGCAGTGCC 2747 TCCCATGTGGGTGGACAATGTTCAGTGTCCAAAAGGACCTGACACGCTGTGGGCAGTGCC 3695 TGTCTGCCCCATGGGAGGGAAGAATCTCCCAGCCCAGCAGAAGAGACCTGGATCACATGTG 3755, AAGATAGAATAAGAGTGCGTGGAGGAGACACCGAGTGCTCTGGGAGAGTGGAGATCTGGC TGTGTCAGCAGCTGGGCTGTGGCTGTGGCTGCCCTGAGGGACGCTTCGTTTGGCC GGGACTGTCACGCCAAACCCTGGGGACAGAGTGACTGTGGACACAAGGAAGATGCTGGCG -- ATCACTGAATGCCTCCT CAGGTCATTTAGCACTTATTTATCCAGTATCTTTGGGCTCCTTCTCCTGGTTCTGTTTA TTCTATTTCTCACGTGCTGCCGAGTTCAGAAACAAAAAACATCTGCCCCTCAGAGTTTCAA 4217 CCAGAAGGAGGGGTTCTCTCGAGGAGATTTATTCCATGAGATGGAGACCTGCCTCAAGA CGGCTGGGACCTGAGCGATGCCCACGTGGTGTCTCAAAAGCTGGGCTGTGGAGTGGCCTT TGAGGTGCTCTGGACAGTCGCTGAA-----3516 3636 3875 3935 3995 2447 2567 2687 4055 3227 3216 3336 4097 4157 , D Qy Db q g δ g a Dρ à ŏ Ω δy Q à g οy qq ò qq δ g ò qq QΩ a ò g δy Db δŽ οy çλ ·δ Óγ ò

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Submitted (14-JUN-1993) Kingsley K.J. Micklem, Nuffield Department
of Pathology, University of Oxford, Level 1, Maternity Block, John
Radcliffe, Hospital, Headington, Oxford, Ox3 9DU, United Kingdom
2 (bases 1 to 3802)
Law,S.K., Micklem,K.J., Shaw,J.M., Zhang,X.P., Dong,Y., Willis,A.C.
                                                                                                                                                                          PRI 22-NOV-1996
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new macrophage differentiation antigen which is a member of the
3344 CAAGAGGAGAACTTAGTCCACCAAATTCAATACCGGGAGATGAATTCTTGCCTGAATG 3403
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                                                                                                                                                                                          H.sapiens mRNA for M130 antigen extracellular variant.
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/protein_id="CAA80544.1"
/db_xref="GI:312148"
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Eur. J. Immunol. 23 (9), 2320-2325 (1993)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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ACCESSION
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KEYWORDS
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TITLE
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AUTHORS
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                                                                                                                       107 GCTACTTGAAGACTCTGGATCTGCTGACTTCAGAAGACATTTTGTCAACCTGAGTCCCTT
                                                                                                                                                                                                           167 CACCATTACTGTGGTCTTACTTCTCAGTGCCTGTTTTGTCACCAGTTCTTTGGAGGAAC
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                                                                                                                                                                   1062 AACCGTCAATTTTGACTGTCTTCATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGC
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  Length 3802;
                                          Indels 123;
  6
                                          Mismatches 1128;
  DB
Score 1339.2;
Pred. No. 0;
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28.9%;
63.5%;
                                          Conservative
Query Match
Best Local Similarity
Matches 2179; Conserv
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Oy GD	2019	CAGTGGGTGGGGAAATAATGACTGCAGTCACAGAGATGTTGGAGTGATCTGTTCTGA 2078 	
0y Dp	2079	TGCATCGGATATGGAGCTGAGGCTGGGAGGGAGCAGCAGGTGCTGCTGGAAAAGTTGA 2138 	
oy Og	2139	GGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAATGGCTGGGGAATGAACATTGC 2198 	•
oy Op	2199	TGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCAGAGAGCCTCA 2258 	
0y 0p	2259	TTTCACAGAAGAACATTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGGAAGC 2318 	
oy B	2319	CTCTCTCTGGGATTGTATACGATGGGAAACAGACTGCGTGTCATTTAAATATGGA 2378 	
Oy Dp	2379	AGCAAGTITGATCTGCTCAGCCCAGGCAGCCCAGGCTGGTTGGAGCTGATATGCCCTG 2438	
Qy Dp	2439	CTCTGGACGTGTTGAAGTGAAACATGCAGACACGGCGCTCTGTCTG	
Qy Dp	2499	CTCTCTTCATGCTGCCAATGTGCTGCAGAAATTAAATTGTGGAGATGCCATATCTCT 2558 	
Qy Dp	2559	TTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCAGTG 2618 	
Oy Dp	2619 1727	TGAAGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAACATCCGGAAGACACTTG 2678	
oy Og	2679	TATCCACAGCAGAGAAGTTGGAGTTGTCTG	
ογ	2709	2708	
q	1847	TGGTTCTTATACTGTGAAAGGGACAGGGTTAGGGAGTCATAGCTGTCTTTTTCTAAAGCC 1906	
Oy Dp	2709	TTCCCGATATACAGATGTCCGACTTGTGAATGGCAAATCCCAGTGTGAGGG 2759  CTGTCTCCTTCCAGGATACACAGAAATTCGCTTGGTGAATGGCAAGACCCGTGTGAGGG 1966	
Oy Dp	2760 1967	GCAAGTGGAGATCAAGGTGCTTGGACACTGGGGCTCACTGTGTGACACCCACTGGGACCC 2819	
Oy Dp	2820	AGAAGATGCCCGTGTTCTATGCAGACAGCTCAGGGACTGCTCTCTCT	
Qy Dp	2880	AGGAAAATATTGGAGAAAGAGGTGTTCGTGTGTGGGGACACAGGTTTCATTGCTTAGG 2939 	
Oy Dp	2940	GAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCTTGGAGCACCTCCCTGTATCCA 2999 	

2386 3419 2626 2686 2866 3839 3046 3959 3,166 4019 3226 AGAGCAAGTGGCCTCTGTAATCTGCTCAGGAAACCAGTCCCAAACACTGTCCTGGAA 2266 3119 2326 3179 2446 CGTGGTGTGTGAAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGTCTCTGCTCACTT 3299 3359 2566 AGGGGTCATCTGCTCAGAATTCACAGCCTTGAGGCTCTACAGTGAAACTGAAACAGAGAG 3479 CTGTGCTGGGAGATTGGAAGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAA 3539 2746 3720 CTCCAGCCCAGCAGAAGAGCTGGATCACATGTGAAGATAGAATAAGAGTGCGTGGAGG 3779
2927 GGCCAGCCCTCGGAGGAGACCTGGATCACATGTGACAAGATAAGATTCAGGAAGG 2986 3106 3239 3,899 4,121 regaaatactetetetetetetecacaggaageeteacccagecatettecatecet 3059 CGCAAATGTATCTGACCCATATTTGTCTGCAGTTCCAGAGGGCAGTGCTTTGATCTGCTT AGAGGACAAACGGCTCCGCCTAGTGGATGGGGACAGCCGCTGTGCCGGGAGAGTAGAGAT CTATCACGACGGCTTCTGGGGCACCATCTGTGATGACGGCTGGGACCTGAGCCGATGCCCA AGACACCGAGTGCTCTGGGAGAGTGGAGATCTGGCACGCAGGCTCCTGGGGGCACAGTGTG TGATGACTCCTGGGACCTGGCCGAGGCGGAAGTGGTGTCAGCAGCTGGGCTGTGGCTC TGCTCTGGCTGCCCTGAGGGACGCTTCGTTTGGCCAGGGAACTGGAACCATCTGGTTGGA TGACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCACGCCAAACCCTGGGG CTTGTGGCAGTGCCCTTCCCGCGGGCTGGGGCAGCACGACTGCAGGCACACGAGGAGGACGC ACAGAGTGACTGTGGACACAAGGAAGATGCTGGCGTGAGGTGCTCTGGACAGTCGCTGAA 2207 2327 2387 3240 2447 3360 3420 3480 2807 3780 2987 3840 3047 3900 3960 3060 3120 3180 3107 3167 4020 3227 4080 3000 qq Q QQ δ qo :: ò g ò g ά qq δ QQ φ qq δ qq Qγ Dp οy qq ò Q ò В δ Ω ò QΩ ò g ò Ω à g ò

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type B superfamily; transmembrane protein type I"
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CGVAQSIPEGAHFGKGAGQVWSHMFHCTGTEEHIGDCLMTALGAPTCSEGQVASVICS
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ANSSAGSGYIMMDKVSCTGNESALWDCKHDGWGKHNCTHEKDAGVTCSDGSNLEMRLV
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Schaer,D.J., Boretti,F.S., Hongegger,A., Poehler,D., Linnscheid,P.
Staege,H., Muller,C., Schoedon,G. and Schaffner,A.
Molecular cloning and characterization of the mouse CD163
Moncloque, a highly glucocorticoid-inducible member of the
scavenger receptor cysteine-rich family
Immunogenetics 53 (2), 170-177 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="macrophage hemoglobin scavenger receptor
                                                                                              3347 CGGGATCCTTGGGGTTGTTCTGTTGGCCATTTTCGTCGCATTATTCTTCTTGACTAAAAA
GAAAACCCCACAAAAAGCCACAAACAGGTCGTCATCTCCTTTATTGCAGT
                                                                                                                                              4182 TCAGAAACAAAAAAATCTGCCCCTCAGAGTTTCAACCAGAAGGAGGGGTTCTCTCGAGGA
                                                                                                                                                                         3407 GCGAAGACAGAGACA---GCGGCTTGCAGTTTCCTCAAGAGGAGAGAACTTAGTCCACCA
                                                                                                                                                                                                                               GAATTTATTCCATGAGATGGAGACCTGCCTCAAGAGAGGAGCACCACATGGGACAAGAAC
                                                                                                                                                                                                                                                         3464 AATTCAATACCGGGAGATGAATTCTTGCCTGAATGCAGATGTAGTGTGGACCTAATGAATTC
                                                              CAGTATCTTTGGGCTCCTTCTCTGGTTCTGTTTATTCTATTCTCTCACGTGGTGCCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="15.43 centirays distal from;the D6Mit300"
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Schaer, D.J., Boretti, F.S. and Schaffner, A.
Direct Submission
Submitted (03-JUN-2000) Departement of Wilder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAK16065.1"
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/note="FAT; member of
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Mammalia; Eutheria; Rodentia;
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KEYWORDS
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HSHGWGRHNCRHKEDAGVICSEFMSLRLTNEAHKENCTGRLEVFYNGTWGSIGSSNMS
PTTVGVVCRQLGCADNGTVKPIPSDKTPSRPWWVDRVQCPKGVDTLWQCPSSPWKQRQ
                                                                                            ASPSSQESWIICDNKIRLQEGHTDCSGRVEIWHKGSWGTVCDDSWDLNDAKVVCKQLG
CQQAYKALKRAAFGPGTGPTHJABLIKCKGNESSLWDCPAKPWSHSDCGHTEDASIQCL
CKGMSESHHGTGHPTLALLVCGAILLVLIYFILWTLKRRRIQRLTVSSRGEVLHQ
VQYQEMDSKADDLDLLKSSGVIQRHTEKENDNL"
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GNQSQTLLPCSSLSPVQTTSSTIPKESEVPCIASGQLRLVGGGGRCAGRVEVCHEGSW
GTVCDDNWDMTDANVVCKQLDCGVAINATGSAYFGEGAGAIWLDEVICTGKESHIWQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAACTGCGACTAGCAGATGGAAGTAACAATTGTTCAGGGAGAGTAGAGGTGAGAATTCA 1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1428 TTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGT---CGGGGCTCATAGCCCCTGTTA 1484
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                                                                                                                                                                                                                 3220. 3288
/note="Region: transmembrane domain"
884 c 1246 g 1101 t
                                                                                                                                                                                                                                                                                                                                       27.5%; Score 1270.4; DB 10
llarity 63.6%; Pred. No. 3.8e-306;
Conservative 0; Mismatches 1131;
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GTGGGGAAAGCATTACTGTCATCATAGAGAAGACGCTGGTGTGACATGTTCTGATGGAGG GGATATGGACGTGAGGTTGTGGGAGAGCAGCAGGTGGTGCTGGAAAGTTGAGGTGAA [11
CTGGGATTGTATACGATGGAGTGGAAACAGACTGCGTGTCATTTAAATATGGAAGCAAG 
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TCATGCTGCCAATGTGCTGTGCAGAGAATTAAATTGTGGAGATGCCATATCTCTTTCTGT
CAGCAGAGAAGTTGGAGTTGTCCCGATATACAGATGCCGACTTGTGAATGGCAA  [1111
CACCCACTGGGACCCAGAAGATGCCGGTGTTCTATGCAGACAGCTCAGCTGTGGGACTGC
TCTCTCAACCAGGGGGGAAAATATTGGAGAAAGAAGTGTTCGTGTGGGGACACGG   1
GTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATCACAGTTCTTGGAGC 
ACCTCCTGTATCCATGGAAATACTGTCTGTGATCTGCACAGGAAGCCTGACCCAGCC

3101 3161 2327 2687 3818 3227 2207 GGATATGACTGATGCCAATGTGGTGTGCAAGCAGCTGGACTGTGGCGTGGCAATTAACGC 2387 2447 2507 3461 2627 3641 2807 2867 2987 13047 31.67 3401 2567 3521 2927 1221 3581 CTGTGCAGACAACGGGACTGTGAAACCCATACCTTCAGACAAGACACCATCCAGGCCCAT 2747 3701 3281 | TGCCGGGGAGAGTAGAGATCTATCACGACGCTTCTGGGGCACCATCTGTGATGACGGCTG CAGGCACAAGGAGGACGCAGGGGTCATCTGCTCAGAATTCACAGCCTTGAGGCTCTACAG CTGTGGGGAGAATGGAGTTGTCAGCCTCGCCCTTTATCTAAGACAGGCTCTGGTTTCAT GTGGGTAGATCGTGTGCAGTGTCCAAAAGGAGTTGACACTTTGTGGCAGTGCCCTCGTC CCCATGGGAGCGAAGAATCTCCAGCC----CAGCAGAAGAGACCTGGATCACATGTGAAGA ACCTTGGAAACAGAGACAGGCCCTCCTCCCAGGAGTCCTGGATCATCTGTGACAA TAAGCAGTTGGCTGTGGCCAAGCTGTGAAGGAAGCAGCATTTGGTCCAGG ACTGTTTCCATGCCTCGCAAATGTATCTGACC---CATATTTGTCTGCAGTTCCAGAGGG CAGTGCTTTGATCTGCTTAGAGGACAAAACGGCTCCGCCTAGTGGATGGGGACAGCCGCTG CGCTGGAAGAGTGGAGGTCTGCCACGAGGCCTCTTGGGGCCACCGTCTGTGATGACAATTG GGACCTGAGCGATGCCCACGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTCAATGC CACAGGAACGGAGTCCCACTTGTGCCAGTGCCCTTCCCGCGCGCTGGGGGCAGCACGACTG 1GAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGAAGTCTTCTATAACGGGACCTGGGG GTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCTCCATATGGCAGTGCCTGTCTGC TAGAATAAGAGTGCGTGGAGGAGACACCGAGTGCTCTGGGAGAGTGGAAGATCTGGCACGC \$CAGCAGCTGGGCTGTGGTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTTGGCCAGGG **AACTGGAACCATCTGGTTGGATGACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGA** CTGTCACGCCAAACCCTGGGGACAGAGTGACTGTGGACACAAGGAAGATGCTGGCGTGAG GTGCTCTGGACAGTCGCTGAAATCACTGAATGCCTCCTCAGGTCATTTAGCACTTATTTT ATCCAGTATCTTTGGGCTCCTTCTCTGTTCTGTTTATTCTATTTCTCACGTGGTGCCG 2328 2448 2508 2688 2748 2868 4119 3045 2148 2268 2388 3342 2568 3522 3702 2808 3759 2928 3879 2988 3999 3108 3102 3162 3282 3402 3462 2628 3582 3642 3819 3939 3048 4059 δ οý g g δ Q Q q ōλ qq Óγ qq ŏ g Q δ q ŏ g ò qq δy g ò g ò q δ qq Óλ Ω δ qq рp ογ δý δ

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NGTSQCEGQVEMKISGRWRALCASHWSLANANVVCRQLGCGVAISTPRGPHLVEGGDQ
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VICSGFVRLAGGDGPCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAELGCGKAVSVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MALGRHLSLRGLCVLLLGTMVGGQALELRLKDGVHRCEGRVEVK
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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3228 ACTCTTGGTTTGTGGAGCCATTCTATTGGTCCTCCTCATTGTCTTCCTCTGTGGACTC- 3286
                                                                                   --TGAAGCGACGGATTCAGCGACTTACAGTTTCCTCAAGAGGAGGGCGTTGATACA 3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-JAN-1992) P.L.J. Wijngaard, Dept of Immunology, University Hospital, P O Box 85500, 3508 GA Utrecht, THE
                                                          AGTICAGAAACAAAAACAICIGCCCCTCAGAGITICAACCAGAAGGAGGGGITCTCTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wildbard, P.L., MacHugh, N.D., Metzelaar, M.J., Romberg, S., Bensaid, A., Pepin, L., Davis, W.C. and Clevers, H.C. Members of the novel WCl gene family are differentially en subsets of bovine CD4-CD8- gamma delta T lymphocytes J. Immunol. 152 (7), 3476-3482 (1994)
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/db_xref="G1:14"
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/organism="Bos taurus"
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                                                                                                                                                               /strain="indicus"·
/isolate="D409"
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Wijngaard, P.L.J.
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SEFLALRMVSEDQQCAGWLEVFYNGTWGSVCRSPMEDITVSVICRQLGCGGSGSLNTS
VGLREGSRPRWDLLQCRRMDTSLMQCPSGPWKX SSGSPREBATISCEGRRPKSCPTA
AGTRDEEKLRELRGGDSECSGRPWHNGSWGTVCDDSWSLARAEVCQQLGCGQALEA
VRSAAFGPGNGSIWLDEVQCGGRESSLMDCVAEPWGQSDCKHEEDAGVRCSGVRTTLP
                                                                                                                                                                                                LABAVYEELDYLLTQKEGLGSPDQMTDVPDENYDDAEEVPVPGTPSPSQGNEËEVPPE
KEDGVRSSQTGSFLNFSREAANPGEGEESFWLLQGKKGDAGYDDVELSALGTSPVTFS
GCGEALNATGSAHFGAGSGPIWLDDLNCTGKESHVWRCPSRGWGRHDCRHKEDAGVIC
                                                                                                                                                                    TTTAGTRTTSNSLPGIFSLPGVLCLILGSLLFLVLVILVTOLLRWRAERRALSSYEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 TCTGGGTTTGAGGCTAGTGGAAGAACAACTCCTGTTCAGGGAGAGTGGAAGTT 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 783 AACTIGITATGATAGTAGTGATCTTGAACTAAGGCTTGTAGGTGGAACTAACCGCTGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 AGGGCGAGTAGAAGTGCATTCTGGAGAAGCTTGGATCCCAGTGTCTGATGGGAACTTCAC
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Pred. No. 2.8e-210;
0; Mismatches 1527;
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2495 2555 2231 2675 2735 2792 2471 2852 2531 2591 2972 3032 2711 2771 3212 3272 3332 3011 3392 2375 2057 TCTTTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCA 2615 2351 2411 2912 2651 CCTGACCCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTTGTCTGCAGT 3092 TCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGGATGGGGA 3152 2831 2891 2951 3071 CTCACTGTGTGACACCCACTGGGACCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAG AGTICTIGGAGCACCICCTGTAICCAIGGAAAIACTGTCTGTGAICTCCACAGGAAG AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAAACAGACTGCGTGTCATTTAAATAT CTTCACACTCCCCACTGCCCAGGTCATCTGTGCAGAGCTGGGAAGGTGGGCAAGGCTGTGTC CTGTGGAGTCGCCATCTCCACCCCCAGAGGACCACATTGGTGGAAGGAGGTGATCAGAT CCTGAACTGCACAGGAACGGAGTCCCACTTGTGGCAGTGCCCTTCCCGCGCGCTGGGGGGCA AGATGCAGGAGTCATCTGCTCAGGATTTGTGC-----GTCTGGCTGGAGGAGAGAGACC CTGCTCTGGACGTGTTGAAGTGAACATGCAGACACATGGCGCTCTGTGTTCTGATTCTGA <u> ĊTGCTCAGGGCGAGTAGAAGTGCATTCTGGAGAAGCCTGGACCCCAGTGTCTGATGGAAA</u> TITCICICITCATGCTGCCAATGTGCTGTGCAGAGAATTAAATTGTGGAGATGCCATATC **ĠTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAACATCCGGAAGACAC PTGTATCCACAGCAGAGAGTTGGAGTTGTCTGTTCCCGATATACAGATGTCCGACTTGT** TCACGGCTGGGACCTGAGCGATGCCCACGTGGTGTCAAAAGCTGGGCTGTGGAGTGGC **CTICAATGCCACGGTCTCTGCTCACTTTGGGGÁGGGGTCAGGGCCCCATCTGGCTGGATGA** GGAAGCAAGTTTGATCTGCTCAGCCCACAGGCAGCCCAGGCTGGTTGGAGCTGATATGCC 2316 2172 2676 2736 2412 2793 2472 2532 2592 2652 3093 3153 1998 2058 2436 2496 2556 2232 2616 2292 2352 2853 2913 2973 3033 2712 2772 2832 3213 2892 3273 3333 2952 3012 Ω g δý g ò g δy Op δy qq ò q δ d ÓΥ g ΩŸ qq Óγ ΩQ δ OD δ Ωp ò qq δ g ά g ò g Qγ a δλ

Melbourne, Cn Australia Loca Source 1. Adb_ Adb_	CDS (1.2)  (1.2)	AGSG AGWI AGWI RCRN WGTI CPSQ AGVI SGAA BASE COUNT S12 a ORIGIN OUGTY MATCh	Sim. 9; CGC; ACC; AAAT; AAAT; ACT;	124 2653 184 2713	Db 242CAGAAGTC Qy 2770 ATCAACGTGCTTGGA Db 295 ATGAATATTTCTGGA Qy 2830 CGTGTTCTATGCAGA Qy 2890 ATTGGGAAAGAGT Qy 2890 ATTGGGAAAGAGT Qy 2890 ATTGGGAAAGAGT Qy 2950 CTTCTGGAAAGAGT Qy 2950 CTTCTGGAAACTGT Qy 2950 CTTCTGGATAACTGT Qy 2950 CTTCTGGATAGTGT Db 475 TTTCTGTGGATAGTGT Db 475 TTTCTGTGGATTGTG
QY         3393         GCACGACTGCAGGCACAAGGACGCAGGGTCATCTGCTCAGAATTCACAGCTTGAG         3452           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         3513 GACCTGGGGCGCGCGGGGGAGGAGCATCACCACACCACA	QY         3693         CCTGTCTGCCCCATGGGAGGAGCGAAGAATCTCCAGCAGAAGAGACCTGGATCACATG         3752           Db         3366         TCTTCTGGCCCATGGAAATACAGTTCATGCTCTCCAAAGGAGGAAGCCTACATCTCATG         3425           QY         3753         TGAAGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Qy         3825         CTGGGGCACAGTGTGTGATGACTCCTGGGCCGAGGCGGAAGTGGTGTCTCGCA         3884           b         3546         CTGGGGCACCGTGTGCGATGACTCCTGGGCGCAGGGCTGAGGTGGTGTCACCA         3605           Qy         3885         GCTGGGCTGTGCTCTGCTGCTGCTGCTGCTGCTTGGTTTGGCCAGGGAACTGG         3944           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 4005 CGCCAAACCCTGGGGACAGAGATGACTGTGGACACAAGGAAGATGCTGGCGTGAGGTGCTC 4064  DD 3726 TGCGGAGCCCTGGGGGCACAGCGACGAGCACGAGGAGGTGCTCGGTGTGAGGTGCTC 3785  OY 4065 TGGACAGTCGCTGAAATCACTGAATGCCTCTCAGG 4100  1	RESULT 11 AF400115 AF400115 DEFINITION Ovis aries EM4b mRNA, partial cds. ACCESSION AF400115 G1:15217033 VERSTON AF400115 G1:15217033 VERSTON AF400115 G1:15217033 Ovis aries ORGANISM Ovis aries ORGANISM Ovis aries ORGANISM Ovis aries ORGANISM Ovis aries AUTHORS ONE G111, J.W. and Walker, I.D. TITLE JOURNAL Unpublished AUTHORS G111, J.W. and Walker, I.D. AUTHORS G111, J.W. and Walker, I.D

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RICDDSWDLDDARVVCRQLGCGGALNALQFAGLGQGSGPIWLDELNCGGKESHVWR
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RALCASHWSLANANVVCRQLGCGVAISTPRGPHFVEGSDQISTVRFHÇSGVESFL
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GPIWLNDLNCTGNESHVWNCPSRGWGRHDCRHKEDAGVICSEFLALRWVSEDQQC
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                                                                                                     'ganism="Ovis aries"
.xref="taxon:9940"
il_type="CD4+ T cell"
ssue_type="efferent mesenteric lymph"
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                                          cation/Qualifiers 2305
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S.scrofa mRNA for scavenger-receptor protein, 1665bp
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al Similarity 61.6%;
974; Conservative
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Kanan, J.H.C.
Direct Submission
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      TCTGACCCATATTTGTCTGCAGTTCCAGAGGCAGTGCTTTGATCTGCTTAGAGGACAAA
                                                         CAGCTCCGCCTGGTGGACGGGACAGTCCCTGTGCCGGGAGAGTGGAGATCCTCGACCAG
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                                               CGGCTCCGCCTAGTGGGATGGGGACAGCCGCTGTGCCGGGAGAGATCTATCACGAC
                                                                                                                                 3250 CAAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGTCTCTGCTCACTTTGGGGAGGGG
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                                                                                       GGCTTCTGGGGCACCATCTGTGATGACGGCTGGGGACCTGAGCGATGCCCACGTGGTGTGT
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MAM 27-AUG-1997

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1665 bp

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RESULT 12 SSSRP3 LOCUS

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                                                          Euteleostomi;
Sus.
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomiamalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1665)
Kanan, J.H., Nayeem, N., Binns, R.M. and Chain, B.M.
Mechanisms for variability in a member of the scavenger-receptor
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-JUL-1996) J.H.C. Kanan, University College London,
Immunology, Fourth floor, Windeyer Building, Cleveland Street, London WCl 6BT, UK
Location/Qualifiers
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/strain="Slab/b"
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Pred. No. 1.4e-126;
0; Mismatches 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="scavenger-receptor
/protein_id="CAA67708.1"
/db_xref="GI:1480361"
                                                                                                                                                                                                cysteine-rich superfamily
Immunogenetics 46 (4), 276-282 (1997)
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Sus scrofa.
Sus scrofa
Eukaryota; Metazoa; Chordata;
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GACTGTAGGCATCCTAATATACAGACTACAGGACTAAAGGCTTTTCCCCATGATTGGGAT	TGGAGCTGATATGCCCTGCTCT 	ACGIGITGAAGIGAAACAIGCAGACACAIGCGCGCTCTGTCTCTGTGAITCTCTCTCTTTCTCTCTTTTCTCTCTTTTCTCTCTTTTCTC	TCATGCTGCCAATGTGCTGTGCAGAGATTAAATTGTGGAGATGCCATATCTCTTTCTGT	GGGAGATCACTITGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGG 			CAAATCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCTTGGACACTGGGGCTCACTGTG	TGACACCCACTGGGACCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAGCTGTGGGAC		CAGGITTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCTTGG	AGCACCTCCCTGTATCCATGGAAATACTGTCTGTGTGTCTGCACAGGAAGCCTGACCA 	GCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTGTCTGCAGTTCCAGAGGG	CAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGATGGGGACAGCCGCTG	TGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGACGGCTG	GGACCTGAGCGATGCCCACGTGGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTCAATGC 	CACGGTCTCTGCTCACTTTGGGGAGGGTCAGGGCCCATCTGGCTGG	CACAGGAACGGAGTCCCACTTGTGGCAGTGCCCTTCCCGCGGCTGGGGCACCACGACTG	CAGGCACAAGGAGGAGGAGGGTCATCTGCTCAGAATTCACAGCCTTGAGGCTCTACAG
338		2445	2505	2565	2625	2685	2742	2802	2862	2922	2982	3042	3102	3162	3222	3282	3342	3402
qu		Qy	Oy Db	Qy	Oy Op	Oy Dp	Qy Db	QY	oy op	Qy Dp	Qy	Qy Dp	Qy	Oy Dp	çç Q	Qy Dp	QY	Qy Db

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Manmalls; butneris; radarfilli; nominitate, nomer, is namels; butneris; radares; Cataffilli; nominitate, nomer, is also college, is, Amaratunge, H.C., Are, JR., Ayele, M., Banks, T., Barbardunge, H.C., Are, JR., Ayele, M., Banks, T., Barbardunge, H.C., Are, JR., Ayele, M., Bondin, D., Bouck, J., Benton, J., Bireva, M., Brown, E., Brown, M., Bryant, N.P., Bubay, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Burkett, C., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Carder, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D. A., Dalaney, K.R., Deladado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K., Deladado, D., Edwards, C.C., Elaj, C., Escotto, M., Farls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Galls, T., Guevara, W., Garner, T., Garza, N., Gill, R., Garis, F., Harris, K., Harr, M., Haulak, P., Hamilton, K., Harris, C., Harris, K., Huber, J., Hulyk, P., Hamilton, K., Jacobson, B., Jia, Y., Johnson, R., Holloway, C., Hollins, B., Jia, Y., Johnson, R., Holloway, C., Liu, J., Liu, Y., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Maheshwari, M., Mapue, P., Martin, R., Mattindale, A., Martinger, R., Mansey, E., Mawhiney, E., Micchell, T., Mohabbat, K., Morgan, M., Naicher, R., Mans, C., R., Marken, R., Mans, C., R., Mans, M., Mans, C., R., Mans, C., R., Mans, C., R., Mans, C., R., Mans, C., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC131207 202252 bp DNA linear HTG 18-AUG-2002
Homo sapiens clone RPl1-326A16, *** SEQUENCING IN PROGRESS ***, 10
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                 1462 GGTGAGCGAGGACCAGGAGTGTGCCGGGTGGCTGGAAGTTTTCTACAACGGGACCTGGGG 1521
                                                                                                                                                             1522 CGGTGTCTGCCGCAGCCCCATGGAAGACATCACCTTGTCCATGATCTGCAGCAGCTTGG 1581
                                                                                                                                                                                                                                                                                                                                3582 CIGIGGGGAGAAIGGAGIIGICAGCCICGCCCTIIAICIAAGACAGGCICIGGIIICAI 3641
                                                                                                                                                                                                                                                                                                                                                                                    1582 CTGTGGGGACAGTGGAACCCTCAACTCTTCCGTTTCTCTTAGGGAAGGTTCTAGACCCCG 1641
3462 TGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGAAGTCTTCTATAACGGGACCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1642 GTGGGTCGATGGAATCCAGTG 1662
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HTG; HTGS_PHASE1.
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Mammalia; Eutheria;
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KEYWORDS
SOURCE
ORGANISM
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AC131207/c
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AUTHORS
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Direct Subm Unpublished

TITLE JOURNAL

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantla; Pecora; Bovoldea; Bovidae; Caprinae; Ovis.

1 (bases 1 to 2165)
Gill, J. W. and Walker, I.D.
Novel T19 transcripts from ovine CD4+ T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-JUL-2001) Veterinary Science, University of
Melbourne, Cnr Park Drive and Flemington Rd, Parkville, VIC 3052,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72500 TGGAGTTGTCTGTTCCCGTGAGATTTTTAAATAATCTTAATTGGCTGGGGCTAGAGATGG 72441
72680 TGTGCTGTGCAGAGAATTAAACTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTT 72621
                                                                                                                      CGAGITIGGGGCTGGAGCTGATAAGTCATGATCTCTTCTATGGCCTTGTCTCCTCTA
                                                                                                                                                                                                                                                                                                                                  12330 AACGIGCTIGGACACIGGGGTCACIGTGTGACACCCACIGGGACCCAGAAGATGCCGT
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                                    TGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGGGGAGTGAAACTCA
                                                                                                     CCTTGCATTATGCCCCATTGTTCAACATCCGGAAGACACTTGTATCCACAGCAGAGAAGT
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/organism="Ovis aries"
/db_xref="taxon:9940"
/cell_type="CD4+ T cell"
/tissue_type="efferent prescapular lymph"
<1. .1263
/note="T19 multigene family member"
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rtial cds.
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AF400122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 2165)
Gill,J.W. and Walker,I.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:15217046
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NOTE: This is a "working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                    Department
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                                                      Center, Depar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCCCACGCCAGCCCAGGCTGGTTGGAGCTGATATGCCCTGCTCTGGACGTGTTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGCTGTGCAGAGAATTAAATTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length
contig of 5200 bp in length
gap of unknown length
contig of 5575 bp in length
gap of unknown length
contig of 8898 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 17393 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 18709 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 58908 bp in length
                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye: 100% of re Assembly program: Phrap; version 0.990329 Consensus quality: 194619 bases at least Q40 Consensus quality: 196802 bases at least Q30 Consensus quality: 198233 bases at least Q20
                              Direct Submission
Submitted (18-AUG-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 2422 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22812 bp in
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of 36871 bp in
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                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Pred. No. 5.6e-118;
0; Mismatches 2;
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                                                                                                                                                                                                          Center project name: HELB
Center clone name: RP11-326A16
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                             Sequencing vector: Plasmid;
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                           /protein_id="Aak92475.1"
Abs.xref="G1:12217047"
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DGWDLDDARVVCRQLGGGBLNATGSAHFGAGSGPIMLDDLNCAGNESHVMRCPSRGW
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BYCQQQGGCQALEAYRAGTFCFGROSSJWLDBYRCRGRESSLWDCAAEPWGQSDCKHE
EDAGYRCSGYRKTLPEPTPAGTWIHGLERILRSGDLFCGSLTAQERKEPEBFWLVGRS
PGRYVGELLCLGSWGHTFLMSGVQLCRI"
                                                                                        GRHDCRHKEDAGVICSEYLALRMVSEDQECAGWLËVFYNGTWGSVCRSPMDDVTVSII
CSQLGCGDSGSLNTSVGLREGSRPRWIDLIQCRKTDTSLWQCPSGPWKFSSCSPKEEA
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/codon_start=1
/product="EP4a'
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WGGVCRSPMEDITLSIICRQLGCGDSGTLNSSVSLREGSRPRWVDRIQCRKTDSSLWE
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GGSWGTVCDDSWSLAEAEVVCQQLGCGHALEALRDAAFGPGSGSIWLDEVQCRGRESS
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Kanan, J. H., Nayeem, N., Binns, R. M. and Chain, B. M.
Kanan, J. H., Nayeem, N., Binns, R. M. and Chain, B. M.
Cysteiner for superfamily
Immunogenetics 46 (4), 276-282 (1997)
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CGATGACTCCTGGAGCCTGGCAGAGGCCGAGGTGTGTCTCAGCAGCTGTGGCCCA
                                    3900 rgcrcrggccrgagggacgcrrrgrrrggcagggaaccargggaacraggaaccarcrggrrga
                                                         3960 TGACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCACGCCAAACCCTGGGG
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Direct Submission
Submitted (15-JUL-1996) J.H.C..-Kanan, University College
Immunology, Fourth floor, Windeyer Building, Cleveland St
London WCl 6BT, UK
Location/Qualifiers
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S.scrofa mRNA for scavenger-receptor protein, 1316bp.
x99333
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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/cell_type="peripheral blood T lymphocyte"
<1. .126
/nuuber=1
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/code=
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/strain="SLAb/b"
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ORIGIN

4 3232 1186 TGCAGTGCAGGGGCAGGGAGTCCTCCTGTGGGACTGTGCTGCGGGGCCCTGGGGGCAGA 1245 AGTCCCACTTGTGGCAGTGCCCTTCCCGCGGCTGGGGGCAGCACGACTGCAGCACAGG 3412 3653 ACATTCAGTGTCCTAAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCCATGGGAGC 3712 946 GCTGTCCAACTACTGCCCCTGCACAGACAAGAGAAGCTGCGACTCAGGGGAGGAGACA 1005 TCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGATGGGGACAGCCGCTGTGCCGGGAGAG 3172 CTCACTTTGGGGAGGGGTCAGGGCCCATCTGGCTGGATGACCTGAACTGCACAGGAACGG 3352 AGGACGCAGGGGTCATCTGCTCAGAATTCACAGCCTTGAGGCTCTACAGTGAAACTGAAA 3472 3473 CAGAGAGCTGTGCTGGGAGATTGGAAGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCA 3532 3533 GGAGGAACATCACCACAGCCATAGCAGGCATTGTGT3CAGGCAGCTGGGGCTGTGGGGAGA 3592 ---GAGTGCGTGGAGGACA 3784 CCGAGTGCTCTGGGAGAGTGGAGATCTGGCACGCAGGCTCCTGGGGCACAGTGTGTGATG 3844 ATGCCCACGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGTCTCTG 3292 3845 ACTCCTGGGACCTGGCCGAGGCGGAAGTGGTGTGTCAGCAGCTGGGCTGTGGCTCTGCTC 3904 TGGCTGCCCTGAGGGACGCTTCGTTTGGCCAGGGAACTGGAACCATCTGGTTGGATGACA 3964 471 591 GIGGAACCCTCAACTCTTCTCTTTAGGGAAGGTTCTAGACCCCGGTGGGTA 825 531 646 ACCAGGAGTGTGCCGGGTGGCTGGAAGTTTTCTACAACGGGACCTGGGGCGGTGTCTGCC 705 GAATCCAGTGTCGGAAAACTGATAGCTCTCTGGGAGTGTCCTTCTGAAAT TAGAGATCTATCACGACGCCTTCTGGGGCACCATCTGTGATGACGGCTGGGGACCTGAGCG 3713 GAAGAATCTCCAGCCCAGCAGAAGAGACCTGGATCACATGTGAAGATAGAATAA----TGCGGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCACGCCAAACCCTGGGGACAGA 54; 259; Indels 1246 GTGACTGCAAGCATGAGGAGGACGCTGGAGTGCTCTGG 1288 GTGACTGTGGACACAAGGAAGATGCTGGCGTGAGGTGCTCTGG Score 460.6; DB 4; Pred. No. 8.7e-104; Mismatches 259; ö Query Match 10.0%; Best Local Similarity 68.8%; Matches 690; Conservative 3113 292 3173 352 3233 412 3293 472 3353 592 706 991 826 1006 1066 3905 3962 4025 g g ò q ò g ö ò ò ò ò

Search completed: May 12, 2003, 05:29:51 Job time : 8566 secs

us-09-759-130b-379.rst

453.8 9.8 457 9 A1738432 447.4 9.7 449 9 A1609329 446.2 9.6 451 10 AW082879 416.8 9.0 799 13 B1185454 414.4 9.0 429 9 A1278132 408.4 8.8 118 13 B1183796 407.8 8.8 411 9 A1090561	401.4 392.8 392.8 359.4 359.4 359.4 353.8 7.9	354 7.6 930 13 BIB38644 324.2 7.0 705 17 B16308 320 6.9 320 9 A5582301 310 6.7 7.3 13 BIB36459 308.8 6.7 1153 9 AL706449 304.8 6.6 484 14 N94111	29 301.8 6.5 644 13 BIO09838 30 299.2 6.5 653 10 BES02724 31 296.8 6.4 616 13 BIO09795 32 294.8 6.4 310 9 AI472927 33 291.6 6.3 585 14 BQ327934 34 290.4 6.3 408 9 AI288981 35 289 6 6 3 711 14 BO376594	4 6.0 581 14 BQ36812 8 6.0 689 12 BF06504 2 5.9 569 10 BF09802 8 5.8 574 14 BQ327932 2 5.8 452 17 AQ672871 57 5.8 833 9 AL574811 57 5.8 874 13 B1009286 4 5.7 560 13 B1009799 4 5.7 583 14 BQ327909	ALIGNMENTS	AL529439 AL529439 LOCUS AL529439 AL529439 AL529439 AL529439 AL529439 AL529439 AL529439 AL529439 AL529439 ACCESSION ACCESSION AL529439 ACCESSION ACCESSI	Ll W.B., Grubbr,C., Jessee,J. an Full-length CDNA libraries and n Unpublished (2001) Contact. Genoscope Genoscope - Centre National de S BP 191 91006 EVRY cedex - France Email: segrefégenoscope.cns.fr, Location/Qualifiers 1.,999	/organism="Homo saplens" /db_xref="taxon:9606" /clone_ilb="LTI_NFL001_NBC4" /sex=male /tissue_lype="neuroblastoma cells" /lab_host="DH108"
	· .	:						· .
4_p5_4578 1gen Ltd.	Search time 3980 Seconds (without alignments) 18832.340 Million cell updates/sec	32308132				-	results predicted by chance to have a 1 to the score of the result being printed, of the total score distribution. SUMMARIES  ID	AL529439 BG570972 602591546 BQ776070 UT-H-FH0- AL529438 AL529438 AL560994 AL56094 AL995706 qb24e01.x
GenCore vers Copyright (c) 1993 - 20 leic - nucleic search, using sw mod	Run on: May 12, 2003, 02:53:40 ; Search ti (withou tibou 18832.3 Title: US-09-759-130B-379 Perfect score: 4628 Sequence: I gcggccgctcgcgatctagaaa	ole: IDENTI Gapop 161540 er of hits s	Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:* 1: em_estba:* 2: em_esthum:* 3: em_esthum:* 4: em_esthum:* 5: em_estpu:* 6: em_estpu:* 7: em_estpu:* 9: ph_estp:* 10: ch_estp:*		15: em_estfun:* 16: em_estom:* 17: 9D_gss:* 18: em_gss_hum:* 19: em_gss_lnu:* 20: em_gss_ln:* 21: em_gss_ln:* 22: em_gss_ln:* 23: em_gss_ln:* 24: em_gss_ln:* 25: em_gss_ln:* 26: em_gss_ln:* 27: em_gss_ln:* 27: em_gss_ln:* 27: em_gss_ln:*	Pred. No. is the number of results predicted score greater than or equal to the score of and is derived by analysis of the total score score is derived by analysis of the total score and is derived by analysis of the total score of the total score of the total score of the number of the score of t	1 958.2 20.7 999 9 AL5.9439 2 578.8 12.5 582 12 BG570972 c 3 568.2 11.3 581 14 B0776070 c 4 512.6 11.1 554 9 AL5.9438 5 491.4 10.6 940 9 AL5.50994 c 6 489.4 10.6 491 9 AI095706

Tue May

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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oilgo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and corned into the Not I and Eco kv sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://tullength.invitrogen.com" 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GCCTTGAGGCTCTACAGTGAAACTGAAACAGAGCTGTGCTGCGGAGATTGGAAGTCTTC
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                                                                                                                                                                                                                    Length 999;
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و
                                                                                                                                                                                                                   Score 958.2; DB 9;
Pred. No. 6.8e-154;
1; Mismatches 4;
                                                                                                                                                                                                                      20.7%;
Local Similarity 99.3%;
hes 982; Conservative
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Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5, and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGGCATANGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGACGCGCCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                          BG27U972 SR2 bp mRNA linear EST 10-APR-2001 602591546F1 NIH_MGC_79 Homo sapiens CDNA clone IMAGE:4714115 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                Humidan:

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammallais Eutheria; Primates; Catarrhini; Hominidae; Homo.

Motional Institutes of Health, Mammallan Gene Collection (MGC)

Inpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

CLOne distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 576.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                             4164
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                                                                               TTAGCACTTATTTTATCCAGTATCTTTGGGCTCCTTCTCCTGGTTCTGTTTATTCTATTT
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/clone_lib="NIH_MGC_79"
/lab_host="DH10B (T1 phage-resistant)"
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Pred. No. 4.6e-89;
0; Mismatches 2;
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/db_xref="taxon:9606"
                                                                                                                                                           CTCACGTGGTGCCGAGTTCAGAAACAAAA 4193
                                                                                                                                                                                198 g
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ilarity 99.7%;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
COMMENT
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BG570972
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KEYWORDS
SOURCE
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Martin
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
The Dr. M. Bento Soares, Destribution information can be obtained
The following repetitive elements were found in this CDNA
sequence: 1.39, AT_rich#Low_complexity
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ776070 581 bp mRNA linear EST 26-JUL-2002 UI-H-FH0-bcl-f-19-0-UI.sl NCI_CGAP_FH0 Homo sapiens cDNA clone UI-H-FH0-bcl-f-19-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 581)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: Bone; Vector: pT/T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR 1; Site_2: Not 1;
                                                                                    3590
                                                                                                                                                                         3650
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                                                                                                           361 GCGAAGAATCTCCAGCCAGCAGAAGAACCTGGATCACATGTGAATAAGAGT
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                      TGACATTCAGTGTCCTAAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCCATGGGA
                                                                                                                                                                                                                                                                                                                                            GCGAAGAATCTCCAGCCCAGCAGAAGAGACCTGGATCACATGTGAAGATAGAATAAGAGT
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/tissue_type~"Human Chondrosarcoma Cell Line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3891 CTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTTGG 3932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTATGG 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-H-FH0-bcl-f-19-0-UI"
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BQ776070.1 GI:21984546
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Unpublished (1997)
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tissue(s): Human Grade I Chondrosarcoma Cell Line The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Per vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAMICGGC. The cell line was provided by Dr James Martin from University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL529438 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD006x005 3 prime, mRNA sequence.
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                                                                                                                                                                                                                             TAG_LIB-UI-H-FH0
TAG_TISSUE-Human Chondrosarcoma Cell Line CS8 - Grade 1
containing the following
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Pred. No. 2.9e-87;
); Mismatches 8; Indels 0;
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Best Local
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                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note—"Organ: Drain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-olgo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized Library was constructed by Life Technologies. *Contact: Feng Liang Life Technologies. *Contact: Feng Liang Life Technologies. a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 Http://fullsani: fliang@lifetech.com URL: http://fullsani: 127 g 110 t 19 others
                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 554)
1 (bases
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3711 GCGAAGAATCTCCAGCCCAGCAGAAGAGACCTGGATCACATGTGAAGATAGAATAAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 512.6; DB 9;
Pred. No. 9.1e-78;
9; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODD006YOO5"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match
Local Similarity 94.8%;
hes 525; Conservative
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/organism="Homo sapiens"
//db_xref="taxon:9606_pub"
//dlone="Cs01066YE07"
//dlone="Cs01066YE07"
//dlone="taxon:9606_pub"
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//dlone=lib="trII_NFL006_pub"
//dlone=lib="trII_NFL006_pub"
//note="vector: pariener. Five prime end enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA was digested with Not I and eloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies.
Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 8000 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: filiangth.invitrogen.com"

28 a 212 c 279 g 218 t 3 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex - France .
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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AL550994
LTI_NFL006_PL2
Prime, mRNA sequence.
AL550994.1
AL550994.1
GI:12888516
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Homo sapiens
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human.
                                                                                                                                                                         Matches 490;
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AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 491)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortum (info@image.llnl.gov) for further information.
Insert Length: 857 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 446.
Location/Qualiflers
                                            3078
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 3259 GGCTGTGGAGTGGCCTTCAATGCCACGGTCTCTGCTCACTTTGGGGAGGGGTCAGGGCCC 3318
                                                                                                                                                                                                                                                                            3319 ATCTGGCTGGATGACCTGAACTGCACAGGAACGGAGTCCCACTTGTGGCAGTGCCCTTCC 3378
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                                                                                                     GGCACCATCTGTGATGACGCTGGGACCTGAGCGATGCCCACGTGGTGTGTCAAAAGCTG
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                                                                                         3079 TATTIGICIGCAGITCCAGAGGGCAGIGCTTIGATCTGCTTAGAGGACAAACGGCTCCGC
                                                                                                                                     CTAGTGGATGGGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGG
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/db_xref="taxon:9606"
/clone="IMAGE:1697208"
/clone_11b="Soares_pregnant_uterus_NbHPU"
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AI095706.1 GI:3434682
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 2959
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AI738432 457 bp mRNA linear EST 21-DEC-1999 wi23906.xl NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391130 3',
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                                                                                                                                                                                                                                                                                                             Score 489.4; DB 9; Length 491;
Pred. No. 8.7e-74;
); Mismatches 1; Indels 0
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
/dev_stage="adult"
/lab_host="DH10B"
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AI738432
AI738432.1 GI:5100413
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99.8%;
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Euteleostomi;

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contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/lmage/limage.html
Insert Length: 631 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 415
                                                                                                                             1 (bases 1 to 449)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                           Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                         Chordata;
                                                                                                               Primates;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                             /note—"Organ: colon; vector: pT7T3D-pac (Pharmacia) with a modified polylinker: Site.1: Not 1: Site_2: Eco RI; plasmid DNA from the normalized library NCI_GCAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1057416-1061255, and 1144984-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI609329 449 bp mRNA linear EST 14-MAY-1999 tw30b02.xl NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2261163 3', mRNA sequence.
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                                                                                                                 information can be
                    Emmert-Buck, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 TGCCTCTGAAGCCACAAAATGACTTTAGACTTCCAGGGCTCACCAGGCTCAAAT
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                                                  cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequenching by: Washington University Genome & Clone distribution: NGT-CGAP clone distribution found through the I.M.A.G.E. Consortium/LINL at: www-bio.lnl, gov/bbrp/image/image.html
Insert Length: 600 Std Error: 0.00
Seq primer: -40UP from Glbco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
  Email: cgapbs-r@mail.nih.gov
Iissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 453.8; DB 9;
Pred. No. 1.1e-67;
                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_CO16"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                  /organism="Homo sapièns"
/db_xref="taxon:9606"
/clone="IMAGE:2391130"
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AI609329/C
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/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; This library represents the normalized version of NOI_CGAP_Ov23. Cloned unidirectionally. Primer: Olgo GT. Average insert size 0.86 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Constructed by Life Technologies."
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                                                                               /tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                Score 447.4; DB 9
Pred. No. 1.3e-66;
0; Mismatches 1
                                        /clone="IMAGE:2261163"
/clone_lib="NCI_CGAP_0v35"
/organism="Homo sapiens"/db_xref="taxon:9606"
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AAATAACATTTCTTGAACAATAGGAGAACAGCTAAATTGATAAAGACTGGTGATAATAAA 4557
211 GCCACAAAATGACTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAG 152
                                                                   BI185454
BI185454.1 GI:14659863
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Best Local Similarity 71.1%;
Matches 564; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: dpomp@unl.edu
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Sus scrofa
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BI185454
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                                                                                                                                                                       EST 14-0CT-1999
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                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 451)
                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4378 GCCACAAAATGACTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAG 4437
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Gaps
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                                                                                                                                                                     AWO82879 451 bp mRNA linear EST
xb71g11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2581796 3', mRNA sequence.
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Pred. No. 2.1e-66;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_wref="taxon:9606"
/clone="IMAGE:2581796"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                   ATAAAAATTGAATTATGTATATCACTGTT 4581
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                         AW082879.1 GI:6038031
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Unpublished (1997)
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AW082879/c
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TITLE
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/db.xref="taxon:9823"
/clone="UNL-P-FN-cw-d-01-0-UNL"
/clone="UNL-P-FN-cw-d-01-0-UNL"
/clone="LD="UNL-P-FN"
/dav_stage="ADDILT"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="Site_1: Not I; Site_2: Eco RI; The UNL-P-FN polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN library is a normalized library representing porcine ovarian follicles, ranging between 2.0 to 10.0 mm in diameter, collected during 7 days of the follicular phase of the pig estrous cycle: This library was derived from the library UNL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the Not I site and the nucleotides present between the nucleotides present b
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BI185454 1799 bp mRNA linear EST I UNL-P-FN Sus scrofa cDNA clone UNL-P-FN-Cw-d-01-0-UNL 3', mRNA sequence.
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Pred. No. 1.7e-61;
0; Mismatches 228;
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by Bonaldo, Lennon and Soares,
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/organism="Sus scrofa"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through
INAGE Consortium (infoétmage.lin1.gov) for fu
INSERT Length: 1693 Std Error: 0.00
Seg primer: -40UP from Gibco.
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9.0%;
Best Local Similarity 99.3%;
Matches 427; Conservative (
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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                                            8 CTGCTCAGGGAACCAGAGTCAGACACTATCCCCGTGCAATTCATCATCTCGGACCCATC
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ORGANISM

REFERENCE

TITLE

VERSION KEYWORDS SOURCE

ACCESSION

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EST 10-JUL-2001
clone
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Pred. No. 5.8e-61;
0; Mismatches 1;
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A1090561 411 bp mRNA linear EST 18-AUG-1998 qa64g07.xl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1691580 3', mRNA sequence.
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/lab_host="HIOB (amptcillin resistant)"
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 411)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                               GAAGAATCTCCAGCCCAGCAGAAGACCTGGATCACATGTGAAGATAGAATAAGAGTGC 3772
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/sex="unknown"
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AI090561.1 GI:3429620
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPHL19W
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// Aca_most_ Action (Laire recumblogues)
// Accessive (Laire action)
// Ac
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                                                                                                                         Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'strain="University of Nebraska, Lincoln Swine Selection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCACTTTGGGGAGGGGTCAGGGCCCATCTGGCTGGATGACCTGAACTGCACAGGAACGG 3352
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Caetano, A.R., Johnson, R.K. and Pomp, D.
Generation and sequence characterization of a normalized CDNA
Unpublished (2001)
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Pred. No. 4.9e-60;
0; Mismatches 175; Indels
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/lab_host="DH10B (Life Technologies)"
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/clone="UNL-P-FN-cd-h-08-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dpomp@unl.edu
Jigo-dr track not found, Not I si'
is likely internal to the message.
Seq primer: M13 -29
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Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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/organism="Sus scrofa"
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    BI183796.1 GI:14658205
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Best Local Similarity 74.5%;
Matches 511; Conservative
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AUTHORS
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/tissue_type="hypernephroma"
/tab_host="DH10B (T1 phage-resistant)"
/hote="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF132072 48.3 bp mRNA linear EST 24-OCT-2000 601821079F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052947 5',
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S NIH-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: agaps-remail.nlh.gov

Tissue Procurement: ATC.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genemics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov now: n column: 20
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                                                                                                                                                                 CATGAGATGGAGACCTGCCTCAAGAGAGACCCCACATGGGACAAGAACCTCAGATGAC
                                                                                                                                                                                                                                               ACCCCCAACCATGGTTGTGAAGATGCTAGCGACACATCGCTGTTGGGAGTTCTTCCTGCC
                                                                                                                                                                                                                                                                                                                             TCTGAAGCCACAAAATGACTTTAGACTTCCAGGGCTCACCAGGATCAACCTCTAAATATCT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 411;
                                          Indels
  6
                                       7
Score 407.8; DB 9
Pred. No. 7.8e-60;
                                          0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:4052947"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BF132072
BF132072.1 GI:10971112
  8.88;
99.58;
                                          Matches 409; Conservative
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                     Similarity
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  Query Match
Best Local :
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AUTHORS
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BF132072
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606 bp mRNA linear EST 27-MAR-2002 UI-1-BB1p-auu-d-07-0-UI.sl NCI_CGAP_P16 Homo sapiens cDNA clone UI-1-BB1p-auu-d-07-0-UI 3', mRNA sequence. BQ024006 BQ024006 I GI:19759285
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs:r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
CONA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
sequence: 5'-ATTCTAGAGGCGGAGGGGCGCCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 606)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                             4260
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                                                                                                                                                                                                                                          4050 TGGCGTGAGGTGCTCTGGACAGTCGCTGAAATCACTGAATGCCTCCTCAGGTCATTTAGC 4109
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                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------TITCAACCAGAAGGAGGGGTTCTCTCGAGGAGAATTTATTCCATGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGACCTGCCTCAAGAGAGAGGACCCACATGGGACAAGAACCTCAGATGACACCCCCAAC
                                                                                                                                                                                                        30;
                                                                                                                                                                    DB 12; Length 483;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                    GTGGTGCCGAGTTCAGAAACAAAAACATCTGCCCCTCAGAG----
                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                   8.7%; Score 401.4; DB 93.6%; Pred. No. 9e-59; Live 0; Mismatches
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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ATA 483
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                                                                                                                                                                    Query Match
                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
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BQ024006/c
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                                                                                                                BASE COUNT
ORIGIN
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                                                                                                                                                                                                        Matches
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COMMENT
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KEYWORDS
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/dew_stage="Full Term"
/dew_stage="Full Term"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Placenta; Vector: pT773-Pac (Pharmacia) with
a modified polylinker; Site_1: EcoR I; Site_2: Not I;
a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCL_CGAP_P16 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        first-strand cDNA contains a library tag sequence that i
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are GA, AGGAA. For
additional information, contact: Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4256 AGATGGAGACCTGCCTCAAGAGAGGACCCACATGGGACAAGAACCTCAGATGACACCC 4315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4316 CCAACCATGGTTGTGAAGATGCTAGCGACATCGTTGGGGAGTTCTTCCTGCCTCTG 4375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAAATAACATTTCTTGAACAATAGGAGAACAGCTAAATTGATAAAGACTGGTGATAATA 4555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4196 ATCTGCCCCTCAGAGTTTCAACCAGAAGGAGGGGTTCTCTCGAGGAGAATTTATTCCATG 4255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4376 AAGCCACAAAATGACTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGA 4435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_TISSUE-placenta human full term
                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="VI-1-BBlp-auu-d-07-0-UI"
/clone_lib="NCI_CGAP_P16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
                                                                                                                                                                                                                                   tissue_type="Placenta
                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAG_LIB=UI-1-BBlp
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Search completed: May 12, 2003, 06:24:01 Job time : 4026 secs

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Sequence 1 Sequence 1 Sequence 1

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Sequence 147, Sequence 147, Sequence 113,

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Sequence

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Sequence

Sequence 1

Sequence

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Run on:

Minimum DB Maximum DB

Database

Searched:

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61 TTTGGAAGATGCTGCTGTCATCAGAACCTTTTCTCTGCTGTGGTAACTTGCATCCTGCTC 120
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CURRENT APPLICATION NUMBER: US/10/042,431

CURRENT FILING DATE: US 09/333,159

PRIOR FILING DATE: 1999-06-14

PRIOR FILING DATE: US 09/578,063

PRIOR FILING DATE: 2000-05-24

NUMBER: OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCGCCCCCCCGCATCTAGAATTAGATGATGCTGCCTCAAAAACTCGTGGCATATTGAT
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US-09-905-291A-147
US-09-905-291A-147
US-09-907-824-147
US-09-907-824-147
US-09-904-011-147
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US-09-907-914-147
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US-09-907-918-113
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US-09-907-908-147
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10042431 Publication No. US20020182675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCCARTHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 4628; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-042-431-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 379, App
Sequence 10, Appl
Sequence 380, App
Sequence 79, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1712, Ap
Sequence 237, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35432, A
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Sequence 10340,
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9366.838 Million cell updates/sec
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                                                                                                                                                                                                                                                   1 geggeegetegegatetaga.......aaaeggaegegtgggtegae 4628
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2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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                                                                                                                                  May 12, 2003, 02:56:30 ; Search time 614 Seconds
                     GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-759-13B-380
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US-09-867-701-10340
US-09-918-995-32438
US-09-918-995-32438
US-09-796-692-269
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US-10-040-862-269
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US-10-040-862-269
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US-09-917-800A-1712
US-09-925-297-237
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                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            783854 segs, 621352466 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              - nucleic search, using sw model
                                                                                                                                                                                                                                                                                    IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Publication No. US20030022279A1
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Fraser, Christopher
Sharp, John D
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Kirst, Susan J
Mackay, Charles R
Myers, Paul S
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Wrighton, Nicolas
Goodearl, Andrew
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Matches 4628; Conservative
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; ORGANISM: Homo sapiens
US-09-759-130B-379
                                                                                        GGGTCGAC 4628
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TGTCCTAAAACGCATATCTCCATATGGCAGTGCCTGTCTGCCCCATGGGAGCGAAGAATC 3720 		GENERAL INFORMATION: APPLICANT: MCCARTHY, Sean A APPLICANT: BARNES, Thomas M ADDITANN: EDASTED Origination	
TCCAGCCCAGCAGAAGAGCTGGATCACATGTGAAGATAGAATAAGAGTGCGTGGAGGA 3780 		APPLICANT: STRARP, CALLS COPIES C. APPLICANT: STRARP, JOHN D. TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC, TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES	
GACACCGAGIGCICIGGGAGAGIGGAGAICIGGCACGCAGGCICCIGGGGCACAGIGIGI 3840 		CURRENT APPLICATION NUMBER: US/10/042,431 CURRENT FILING DATE: 2001-10-25 PRIOR APPLICATION NUMBER: US 09/333,159	
GATGACTCCTGGGACCTGGCCGAAGCGGAAGTGGTCTCAGCAGCTGGGCTGTGGCTCT 3900 		PRIOR FILING DATE: 1999-00-14 PRIOR APPLICATION NUMBER: US 09/578,063 PRIOR FILING DATE: 2000-05-24 PRIOR PILING DATE: 2000-05-24	
GCTCTGGCTGCCCTGAGGGACGCTTCGTTTGGCCAGGGAACTGGAACCATCTGGTTGGAT 3960 			
GACATGCGGTGCAAAGGAAATGAGTCATITCTATGGGACTGTCACGCCAAACCCTGGGGA 4020 	Sn	ORGANISM: Homo Saprems -10-042-431-10  Query Math. 94.2%; Score 4359; DB 9; Length 4359;	
CAGAGTGACTGGACACAAGGAAGATGCTGGCGTGAGGTGCTCTGGACAGTCGCTGAAA 4080 	QV	latches 4359; Conservative 0; Mismatches 0; Indels 0; Gaps 28 ATGATECTECTEAAAACTCGTGGCATATTGATTTTGGAAGATGCTGCTGTCATCAGAAC 87	•
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TAACATTTCTTGAACAATAGGAGAACAGCTAAATTGATAAAGACTGGTGATAATAAAAAT 4560	q <sub>C</sub>	421 GAAGAIGTIGGIGTIGAACIGTIATIGTIGAAGCCAATCTGGGTTTGAGGCTAGTGGATGGA 480	

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110	8 TGCTCAGATGGAGCAGATTTGGAACTGCGACTAGCAGATGGAAGTAACAATTGTTCAGGG 11
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132	1 AATGAGTCAGCTCTGGGACTGCACATATGATGGAAAGCAAAGCGAACATGCTTCCGA 138 AATGAGATCAGATGCTGGGGACTGCACATATGATGGAAAACCAAAGCGAAAGCTAAGGCTTCCGA 138 AGATCAGATGCTGGAGTAATTTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGG 146
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: HOLLZMAN, Douglas A
INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
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PRERENCE: MP100-5350MNIM
APPLICATION NUMBER: US/09/759,130B
FILING DATE: 2002-09-16
PPLICATION NUMBER: US 09/479,249
PPLICATION NUMBER: US 09/479,497
PPLICATION NUMBER: US 09/559,497
ILING DATE: 2000-04-27
PPLICATION NUMBER: US 09/578,063
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Sharp, John D
Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Leiby, Kevin R
Wrighton, Nicolas
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PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
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PRIOR APPLICATION NUMBER: US 09/608,452
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GGCACAGTG	ACTGC	ACTGC	TTTGG	GTGGG	GTGGG	CATCG	TGAAT	TGAAT	AAGTT	AAGTT	TCACA	CTCTC	CTCTC	CAAGT			CTCTT	CTCTT	CTGTG		AAGGG	TCCAC	TCCAC	GCAAA	GCAAA	GTGAC       GTGAC	CTGCT	CIGCI	ACAGG	
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BUBLICATION NO. US20020182675A1

GENERAL INFORMATION:

APPLICANT: MCCARTHY, Sean A

APPLICANT: BARNES, Thomas M

APPLICANT: FRASER, Christopher C

APPLICANT: FRASER, Christopher C

APPLICANT: BARNES, Thomb D

TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

FILE REFERENCE: 10147-602

CURRENT PILING DATE: 2001-10-25

PRIOR PILING DATE: 1999-06-14

PRIOR PLICATION NUMBER: US 09/333,159

PRIOR FILING DATE: 1999-06-14

PRIOR FILING DATE: 1900-05-24

NUMBER OF SEQ ID NOS: 79

SOFTWARE PARENTING PARE: 2000-05-24

NUMBER OF SEQ ID NOS: 79

SEQ ID NO 79

LENGTH: 4308
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Pred. No. 5.5e-233;
0; Mismatches 1527;
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Matches 2061; Conservative
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; ORGANISM: BOS SP.
US-10-042-431-79
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APPLICANT: Barnes, Thomas S
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APPLICANT: Barnes, Thomas S
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
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APPLICANT: Myers, Paul S
APPLICANT: Wighton, Nicolas
APPLICANT: Wighton, Nicolas
APPLICANT: Wighton, NovEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
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                                              GCTGGGCTGTGGCCCAGGCCCTGGAAGCCGTGCGGTCTGCAAGTTTGGCCCTGGAAATGG 3644
                                                                                               3945 AACCATCTGGTTGGATGACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCA 4004
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Pred. No. 5.5e-233;
0; Mismatches 1527;
                                                                                                                                                                                                                                                                                               TGGACAGTCGCTGAAATCACTGAATGCCTCCTCAGG 4100
                                                                                                                                                                                                                                                                                                                                                TGGTGTAAGGACAACATTGCCCACGACCACAGCAGG 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Millennium Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 449
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 449, Application US/09759130B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCarthy, Sean A
Fraser, Christopher
Sharp, John D
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54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20030022279A1 GENERAL INFORMATION:
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Matches 2061; Conservative
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; ORGANISM: Bovine
US-09-759-130B-449
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US-09-759-130B-449
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                              GTGCAGGCAACTAGGATGTCCATCTTTTATTTCTTCTGGAGTTGTTAATAGCCCTGC 662
                                                                                                                                                                                                                                    663 TGTATTGCGCCCCATTTGGCTGGATGACATTTTATGCCAGGGGAATGAGTTGGCACTCTG 722
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CCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGAACTTGAATACTGCTGCCGTGGT
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9 TCCCTGGGCGGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGA 6 CAGTGGACCAAGGAATGCAGCTGTTGTGTGTAAACAATTGGGATGTGGAAAGCCTAT		AAA GCC GAA TTC	6 TGATGCATCGGATATGGAGCTTGAGGTGGAGCAGCAGCAGCTGTGCTGGAAAAGT		GGAAGCAAGTITGAICTGCTCAGCCCACAGCCACCAGGCTGGTTGGAGCTGATATGCC	6 TTTCTCTCTTCATGCTGCCAATGTGCAGAGAATTAAATTGTGGAGATGCCATATC
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2750 2810 3110 2675 2330 2735 2390 2792 2450 2852 2912 2570 2972 3032 3152 3212 2870 3272 3332 2990 3392 3452 3512 3164 3572 3692 2631 IGCCTIGGGTGGGCCTGACTGTTCCCATGGCAACAGCCTCTGTGATCTGCTCAGGAAA 2690 CCTGAACTGCACAGGAAAGGAGTCCCACGTGTGGAGGTGCCCTTCCCGGGGCTGGGGGGCG 3050 CCACACCCAGGTGCTGCCCCAGTGCAACGACTTCCTGTCTCAACCTGCAGGCTCTGCGGC CTCACTGTGTGTGACACCCACTGGGACCCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAG GTGGGGACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATGAC AGTICITGGAGCACCTCCTGTATCCATGGAAATACTGTCTCTGTGATCTGCACAGGAAG TCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGATGGGGA CAGCCGCTGTGCCGGGAGAGATGTATCACGACGGCTTCTGGGGCACCATCTGTGA TGACGCCTGGGCACCTGAGCGATGCCCACGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGC CCTGAACTGCACAGGAACGGAGTCCCACTTGTGGCAGTGCCCTTCCCGCGCGGCTGGGGGCCA GCACGACTGCAGGCACAAGGAGGACGCAGGGGTCATCTGCTCAGAATTCACAGCCTTGAG GCTCTACAGTGAAACTGAAACAGAGCTGTGCTGGGAGATTGGAAGTCTTCTATAACGG GCAGCTGGGGCTGTGGGGAGAATGGAGTTGTCAGCCTCGCCCCTTTATCTAAGACAGGCTC ACAGCTTGGATGTGGGGACAGTGGAAGTCTCAAACACCTCTGTTGGTCTCAGGGAAGGTTC TGGTTTCATGTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCTCCCATATGGCAGTG GTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCCATTGTTCAACATCCGGAAGACAC 2271 GIGIGAIGGGGGGGGAGCCIGAGCICIGGICCIGCCCAGAGIGCCCIGICCAGGAGGCAC G---AATGGCAAATCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCTTGGACACTGGGG CCTGACCCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTTGTCTGCAGT TTGTATCCACAGCAGAGAAGTTGGAGTTGTCTGTTCCCGATATACAGATGTCCGACTTGT 2676 2451 2511 2913 2571 2973 3033 2691 3093 3153 2811 3213 2871 3273 2931 3333 2991 3393 3051 3453 3111 3513 3165 3573 3225 3633 3285 2616 2736 2391 2793 2853 qq qq qq δy  $^{0}$ δ Op Óγ Db δ qq ŏ Вb δλ Q Ω g ò Ω δ q δ pp δy Qγ Dp δ g δ 염 δ Q οy

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; LOCATION: (1)...(473)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-32438
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ilarity 98.9%;
Conservative (
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 437; Conserv
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LENGTH: 473
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                                                          3767 --GAGTGCGTGGAGGACACCGAGTGCTCTGGGAGAGTGGAGATCTGGCACGCAGGCTC
                                                                                                        3465 CCGCCTCAGGGAGGAGAGCAGTGCTCAGGGCGGGTGGAGGTGTGGGCACAACGGCTC
                                                                                                                                                               3885 GCTGGGCTGTGGCTCTGCTGTGCCTGAGGACGCTTCGTTTGGCCAGGGAACTGG
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APPLICANT: Adjate, Paul A.

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

SURRENT FILING DATE: 2001-05-29

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ. ID NO 10340

LENGTH: 449
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Pred. No. 1.1e-112;
0; Mismatches 1;
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                             3753 TGAAGATAGAATAA---
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US-09-867-701-10340
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                           209 CTGAAGCCACAAAATGACTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTT
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                                                                                                                       4373 CTGAAGCCACAAAATGACTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTT
                                                                                            4433 TGAAGGAGACAACAACTTTTAAATGAATAAAGAGGAAGTCAAGTTGCCCTATGGAAAACT
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PLILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
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Pred. No. 3.9e-109;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                  Sequence 32438, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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PRIOR APPLICATION NU
PRIOR FILING DATE: 2
PRIOR APPLICATION NU
PRIOR FILING DATE: 2
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US-09-796-692-269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1890 TAGCCAGCTGGACTGCCCATCTTCTATCATTGGCATGGGTCTGGGAAACGCTTCTACAGG 1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1950 ATATGGAAAATTTGGCTCGATGATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTC 2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1770 GGGCCTGAGGCTGGTGGGGGGGCAGCAACCGCTGGGGAAGACTGGAGGTGTACTTTCA 1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 TAACCAGCTGGGATGTCCAACTGCTATCAAAGCCCCTGGATGGGCTAATTCCAGTGCAGG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 GGAGCTGAGGCTAGTGGATGGTGAAAACAAGTGTAGCGGGAGGTGGAAGTGAAAGTCCA 220
391 IGGATGACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCACGCCAAACCT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 GGAGGAGTGGGAACGGTGTGAATAATGGCTGGAGCATGGAAGCGGTCTCTGTGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 599
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM FO COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 213; DB 9;
Pred. No. 4.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 138:
US-10-040-739-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998 ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                       Sequence 138, Application US/10040739 Patent No. US20020173635A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 498-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                               Merberg, David
Treacy, Maurice
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 599 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                              4016 GGGGACAGAGTGACTGTGGACA 4037
                                                                      McCoy, John
LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                                                    APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 876-56
INFORMATION FOR SEQ ID NO: 138
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
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Best Local Similarity 68.0%;
Matches 297; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF
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APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILLE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/180,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
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                                                                                                         401 TTGCAAACATGATGGGGAAAGCATTATTGCAATCACAATGAAGTGCTGGCGTGAC 460
                                                                                                                                                                                                                                                                                                    2130 AAAAGTIGAGGIGAAIGICCAGGGIGCCGIGGGAAITCIGIGIGCIAAIGGCIGGGGAAI
                                                                             2010 ATGCAGGAACAGTGGGTGGGGAAATAATGACTGCAGTCACAGTGAAGATGTTGGAGTGAT
                                                                                                                                                                           Length 461;
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Pred. No. 2.4e-44;
0; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 269
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APPLICATION NUMBER: 60/200,303
FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,779
FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 269, Application US/09796692 Publication No. US20020198362Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/218,950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-05-01
APPLICATION NUMBER: 60/202,084
FILING DATE: 2000-05-04
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                                                                                                                                                                                                                                                                                                                                                                               GAACATTGCTGAAGTTG 2206
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Best Local Similarity 66.77
Matches 299; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-269
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TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther TITLE OF INVENTION: Hematological Malignancies
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                                                                                                                                                                                                                                                             65 GTGTGATGATAACTTCAACATAGATCATGCATCTGTCATTTGTAGACAACTTGAATGTGG 124
                                                                                                                                                                                                                                                                                                                                                     125 AAGTGCTGTCAGTTTCTCGGTTCATCTAATTTTGGAGAAGGCTCTGGACCAATCTGGTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 TCCAAGGAGAATGGGGGACAATATGTGATGACGGCTGGGACAGTTACGATGCTGTGGG 424
                                                                        Gaps
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                                                                                                                                                               5 TGGAGGGAATATGTGTTCTGGAAGAATAGAGATCAAATTCCAAGGACGGTGGGGAACAGT
                                                                                                                                                                                                                                                                                                       ATTITCTITCGCCATGTTTCGTTTTGGACAAGCCGTGACTAGACATGGAAAAATTTGGCT
                        Length 461;
                                                                        Indels
                        4.3%; Score 199.2; DB 9;
66.7%; Pred. No. 2.4e-44;
11ve 0; Mismatches 148;
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PRIOR PELLING DATE: 2000-03-01
PRIOR AFPLICATION NUMBER: US 60/186,126
PRIOR AFPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR AFPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR PELLOATION NUMBER: US 60/200,999
PRIOR AFPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 269, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
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                                                                        Conservative
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Mannion, Jane
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                                                Similarity
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                                                     Best Local Sin
Matches 299;
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                             Query Match
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: (6)/186,126
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR PRILING NUMBER: 60/190,479
                                                                                                                                                                                     363 TGATGATGTTTCCTGTTA-TGGAAATGAGTCAGCTCTCTGGGAATGTCAACACCGGGAAT 421
                                                                                                                                                                                                                                                                                                                                                                             541
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                                                                                              ATTITCTTTCGCCATGTTTCGTTTTGGACAAGCCGTGACTAGACATGGAAAAATTTGGCT 362
                                                                                                                        GGGGAAGCCATAACTGTTATCATGGAGAAGATGTTGGTGTGAACTGTTATGGTGAAGCCA 481
                                                                                                                                                                                                                                                                                                                          245 GGGGAAAGCATAACTGTGATCATGCTGAGGATGCTGGAGTGATTTGCTCAAAGGGAGCAG 304
                                                                                                                                                                                                             GTGTGATGATAACTTCAACATAGATCATGCATCTGTCATTTGTAGACAACTTGAATGTGG
                                                                                                                                                                                                                                                                                                                                                                          ATCTGGGTTTGAGGCTAGTGGAAGCAACTCCTGTTCAGGGAGAGTGGAGGTGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 TCCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGAACTTGAATACTGCTGCCGTGG
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGCAAGCAACTGGGATGTCCAACTGC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602 TGTGCAGGCAACTAGGATGTCCATCTTC 629
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Publication No. US20020198362A1
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FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,999
FILING DATE: 2000-05-01
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APPLICATION NUMBER: 60/200,303
FILING DATE: 2000-04-28
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FILING DATE: 2000-05-22
APPLICATION NUMBER: 60/218,950
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PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-03-17
APPLICATION NUMBER: 60/200,545
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FILING DATE: 2000-05-04
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TYPE: DNA
CRGANISM: Homo sapiens
US-09-796-692-7354
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GENERAL INFORMATION:
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US-09-796-692-7354
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183 TGGAGACGGTCCCTGCTCTGGGACAGTGGAGGTGAAATTCCAGGGACAGTGGGGGACTGT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 ATTTTCTTTCGCCATGTTTCGTTTTGGACAAGCCGTGACTAGACATGGAAAAATTTGGCT
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APPLICANT: TSURGOCKA, No. US20020160490Aluo
APPLICANT: YAMASHIRO, Kyoko
APPLICANT: YAMAGUCHI, No. US20020160490Alomi
TITLE OF INVENTION: No. US20020160490Alel Serine Protease
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Pred, No. 2.4e-44;
                                                                      PRIOR AFFLICATION NUMBER: US 00/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR PELICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-20
PRIOR PELICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-04
PRIOR PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR PRIOR PRIOR DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/796,692 PRIOR FILING DATE: 2001-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.3%;
Best Local Similarity 66.7%;
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-7354
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US-09-147-947-5
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FURRENT APPLICATION NUMBER: US 60/10/04,862

CURRENT FILING DATE: 2001-11.06

PRIOR FILING DATE: 2000-03-11

PRIOR PELICATION NUMBER: US 60/190,479

PRIOR PILING DATE: 2000-03-17

PRIOR PILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR PILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303
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Pred. No. 2.4e-
0; Mismatches
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2001-09-01
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FASTSEQ for Windows Version 3.0
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ilarity 66.7%;
Conservative (
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-10-040-862-269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 299; Conserv
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LENGTH: 461
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1193 AGTGGTGGACAATATGTGACCAGAACTGGAAGAATGAACAAGCCCTTGTGGTTTGTAAGC 1252
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                                                   GTCAGCTTGGCTACAAGGGTCCTGCCAGAGCAAGAACCATGGCTTACTTTGGAGAAGGAA 1516
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            GCCAGCTGGACTGCCCATCTTCTATCATTGGCATGGGTCTGGGAAACGCTTCTACAGGAT 1951
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                                                                                            ATGGAAAAATTTGGCTCGATGATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCAT
                                                                                                                    CCAGGAACAGTGGGGAAATAATGACTGCAGTCACAGTGAAGATGTTGGAGTGATCT
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GENERAL INFORMATION:
APPLICANT: TAUROKA, NO. US20020160490Aluo
APPLICANT: TAMAGUCHI, NO. US20020160490Aluo
APPLICANT: TAMAGUCHI, NO. US20020160490Aloni
TITLE OF INVENTION: NO. US20020160490Alel Serine Protease
FILE REFERENCE: 001560-349
CURRENT APPLICATION NUMBER: US/09/147,947A
EARLIER FILING DATE: 1997-03-24
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: JP 9/213969
EARLIER FILING DATE: 1997-07-24
MUMBER OF SEQ. ID NOS: 6
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Pred. No. 3.5e-42;
; Mismatches 438;
                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/09147947A ; Patent No. US20020160490A1
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Matches 500; Conservative
                                                                                                                                                                                                                                                            GTTCTGAT 2079
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1637 GTGATTAT 1644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Mouse
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                                                                                                                                                                                                                                                                                                                                                             Score 197.6; DB 9;
Pred. No. 2.1e-43;
0; Mismatches 439;
FILE REFERENCE: 001560-349
CURRENT APPLICATION NUMBER: US/09/147,947A
CURRENT FILING DATE: 1997-03-24
EARLIER APPLICATION NUMBER: PCT/JP98/03324
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                               4.3%;
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Matches 505; Conservative
                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION:
US-09-147-947-5
                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                         Q ID NO 5
LENGTH: 2562
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                           FEATURE:
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1638 GTGTCAAACAAGACATTGGAAGGCACAACTGCCGCCACAGTGAGGATGCAGGAGGTCTT 1697
1101 TGGAGGTCTACTACAAGGGGCAGTGGGGGAACTCTGTGATGATGGCTGGACTGAGATGA 1160
                                                                                                                                                                                                                                                                                                                                                                                          1952 ATGGAAAAATTTGGCTCGATGATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCAT 2011
                                                                   1553 ATGCAGCTGTTGTGTGTAAACAATTGGGATGTGGAAAGCCTATGCATGTGTTTGGTATGA 1612
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| 1698 GT 1699
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Search completed: May 12, 2003, 06:36:37 Job time : 658 secs App11 Appli Appli

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Sequence 3, Appli
Sequence 3, Appli
Sequence 34, Appl
Sequence 33, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                                                              Patent No. 5258287
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                     Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1
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Patent No. 634606
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE REFERENCE: 4121-108
FILE REFERENCE: 4121-108
CURRENT FILIAG DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
FARLIER RILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 197.8; DB 4;
Pred. No. 4e-45;
0; Mismatches 882;
       US-08-232-4631-14
US-09-276-531-129
US-08-628-417-6
US-09-1014-969-14
US-09-801-052-1
US-09-628-417-5
US-09-628-417-5
US-09-628-417-5
US-09-419-459-1
US-08-821-994-64
                                                                                                                                                  US-09-385-982-542
US-09-247-373B-33
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ilarity 48.1%;
Conservative
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; ORGANISM: Homo sapiens
US-09-341-587-4
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Best Local Simmatches 1094;
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Patent No.
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                                                                   ; Search time 103 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                      hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                            nucleic search, using sw model
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                                                                                                           US-09-759-130B-379
4628
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CTTGCCTGCATCGACAGTAGGATCTGAATCCAGTTTGGCCCTGAGGCTGGTGAATGGAGG LDOS CAACCGCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGACGGTGGGGGCACAGTGTGTG 1853	Ţ.
166	
TGACGGCTGGAACAGTAAAGCTGCAGCTGTGGTGTAGCCAGCTGGACTGCCCATCTTC 1913	
TATCATTGGCATGGGTCTGGGAACGCTTCTACAGGATATGGGAAAATTTGGCTCGATGA 1973	
TGTTTCCTGTGATGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGGTGG	
TAATGACTGCAGTCACAGTGAAGATGTTGGAGTGATCTGTTCTGATGC 2081.	
TATGGAGCTGAGGCTTGTGGGTGGAAGCAGCAGGTGTGCTGGAAAAGTTGAGGTGAATGT 2147	
CCAGGGTGCCGTGGAATTCTGTGTGTGTAATGGCTGGGGAATGAACATTGCTGAAGTTGT 2207 	:
TTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCAGAGGCCTCATTTCACAGA 2267 	•
AAGAACATTACACATCTTAATGTCGAAATTCTGGCTGCACTGGAGGGGAAGCCTCTCTG 2327 	· · ·
GGAITGIAIACGAIGGGAGIGGAACAGACIGCGIGICAITIAAAIAIGGAAGCAAGTIT 2387 	
GATCTGCT	
TGCATCAACAGCAGGATCTGAATCCAGTTTGGCCCTGAGGCTGGAAATGGAGGG 2385	
CTGCTCTGGACGTGTTGAAGTGAAACATGCAGACACATGGCGCTCTGTCTG	
TTCTCTCTTCATGCTGCCAATGTGCTGTGCAGAATTAAATTGTGGAGATGCCATATC 2555	
TCTTTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCA 2615	
GTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAACATCCGGAAGACAC 2675	
2676 TTGTATCCACACAGAGAAGTTGGAGTTGTCTGTTCCCGAT	

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                          2686 CAGCCCAGACACTIGGCCAACCICICGIGCAICAACAGCAGGAICIGAAICCACTIIGGC 2745
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                                                               2724 TGTCCGACTTGTGAATGGCAAATCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCTTGG
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APPLICANT: Snyder, Solomon H
TITLE OF INVENTION: Ebnerin: A Secreted von Ebner's Gland
TITLE OF INVENTION: Protein Associated with Taste Buds
TITLE OF INVENTION: Protein Associated with Taste Buds
NUMBER OF SEQUENCES: 6
CORRESPEDINGE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STAFE: D.C.
COUNTRY: USA
ZIP: 20001
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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3193 TTCTGGGGCACCATCTGTGATGACGGCTGGGACCTGAGCGATGCCCACGTGGTGTCTAA 3252
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                                                        1123 AGTGCCCACTTTGGACAAGGCTCTGGATGTTGTTGTTGTTGTGGATGACGTGGCCTGTACAGGA
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Pred. No. 1.2e-28;
); Mismatches 102; Indels
                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER NAPLICATION NUMBER: PCT/DE98/00096
EARLIER PILLING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
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Patent No. 6346606
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Ouery Match
Best Local Similarity 66.4%
Matches 202; Conservative
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CORGANISM: Homo sapiens
US-09-341-587-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2782 GGACACTGGGGCTCACTGTGTGACACCCACTGGGACCCAGAAGATGCCCGTGTTCTATGC 2841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2842 AGACAGCTCAGCTGTGGGACTGCTCTCTAACCAGGAGGAAAATATATTGGAGAAAAGA 2901
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Pred. No. 1.2e-31;
0; Mismatches 324; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,350B
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Wolffe, Susan A
REGISTRATION NUMBER: 33,568
REFERENCE/DOCKET NUMBER: 011C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-929
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 53.3%;
Matches 407; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                  CLASSIFICATION: 435
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94..3963
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                                                                                                                FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-08-470-350B-1
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Best Local S
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                                                                                                                                             304 CAGCTGGGCTGTGGCTGGGCCATGTCGGCCCCAGGAAATGCCCGGTTTGGCCAGGGCTCA 363
                                          3313 GGCCCCATCTGGCTGGATGACCTGAACTGCACAGGAACGGAGTCCCACTTGTGGCAGTGC
                                                                                                                         3373 CCTTCCCGCGGCTGGGGGCAGCACGACTGCAGGCACAAGGAGGACGCAGGGGGTCATCTGC
                                                                               364 GGACCCATTGTCCTGGATGATGTGCGCTGCTCAGGGAATGAGTCCTACCTGTGGAGCTGC
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Pred. No. 1.3e-25;
0; Mismatches 439;
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90 MIDDLEFIELD ROAD, SUITE 200
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CYSTEINE-RICH DOMA:
ANTIBODIES THERETO
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APPLICATION NUMBER: US 60/039,956
FILING DATE: 06-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/034,910 FILING DATE: 04-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09034916
Patent No. 6046314
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: GEBEK, JOHN A.
APPLICANT: STADAY, ANTHONY W.
APPLICANT: ARUFFO, ALEJANDRO A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%;
Best Local Similarity 51.1%;
Matches 499; Conservative
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**MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
OPERATING SYSTEM: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
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CALIFORNIA
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TITLE OF INVENTION:
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; LOCATION:
US-09-034-916-1
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STATE:
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GENERAL INFORMATION:
APPLICANT: MOLICHAUCEr, Jan
TITLE OF INVENTON: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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0; Mismatches 105;
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5.1e-28;
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EARLIER APPLICATION NUMBER: PCT/DE98/00096 EARLIER FILING DATE: 1998-01-09
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Best Local Similarity 66.1%;
Matches 201; Conservative
                                        NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
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US-09-341-587-2
                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-341-587-7
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LENGTH: 2001
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RESULT 8
US-08-473-791-9
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3194 TCTGGGGCACCATCTGTGATGACGCTGGGACCTGA3CGATGCCCACGTGGTGTGTCAAA 3253
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                                                                      490 CCTGGGCATTGCAAGGGACGCGTGGAAGTGAAGCCACCAGAACCAGTGGTATACCGTGTGC
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                                                        -CAGAGAGCTGTGCTGGGAGATTGGAAGTCTTCTATAACGGGACCTGGGGCAGCGTCGGC
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Patent No. 5644035
GENERAL INFORMATION:
APPLICANT: Koths, Kirston E.
APPLICANT: Halenbeck, Robert F.
APPLICANT: Taylor, Eric W.
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APPLICANT: Casipit, Clayton L. TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein NUMBER OF SECUENCES: 11
CORRESPONDENCE ADDRESS:
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                                                                           Corporation
                                                                                                                                                                                                                                                                        07-Jun-1995
07-Jun-1995
08- 530
09- 70- 1995
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/961,404 FILING DATE: 15-0CT-1992 ATTONEY/AGENT INFORMATION: NAME: Goldman, Renneth M. REGISTRATION NUMBER: 34,174
                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN RELEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/316,714
                                                                     ADDRESSEE: Cetus Oncology Corpor
STREET: 1400 Fifty-Third Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
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LENGTH: 2285 base pairs
TYPE: nucleic acid
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Best Local Similarity 62.1:
Matches 187; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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3194 TCTGGGGCACCATCTGTGATGACGGCTGGGACCTGAGCGATGCCCACGTGGTGTGTCAAA 3253
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                                                                                                                                                                                                                                                                     APPLICANT: Casipit, Clayton L. TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,714
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1400 Fifty-Third Street
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                                                                                                                    Sequence 9, Application US/08316714 Patent No. 5965382
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/FILING DATE: 15-0CT-1992
ATTORNEY-AGENT INFORMATION:
NAME: Goldman, Kenneth M.
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SEQUENCE CHARACTERISTICS:
LENGTH: 2285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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(510) 658-5470
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APPLICANT: Wang, Alice M.
APPLICANT: Casipit, Clayt
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Best Local Similarity 62.1
Matches 187; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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; MOLECULE TYPE:
US-08-316-714-9
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             550 ¢ 550
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                                                                                                                      APPLICANT: Wang, Alice M.
APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein NUMBER OF SEQUENCES: 11
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Pred. No. 4.4e-23;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        3: Cetus Oncology Corporation
1400 Fifty-Third Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995
NI: 435
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FILING DATE: 15-OCT-1992
ATORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/316,714
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9, Application US/08473791
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                            Koths, Kirston E.
Halenbeck, Robert
Taylor, Eric W.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  Sequence 9, Applicatic Patent No. 5736340 GENERAL INFORMATION:
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                                                                                                                                                                                                                                        ADDRESSEE:
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APPLICANT: Khodadoust, Mehran et al.
TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
FILE REFERENCE: MNI-073CP
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APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 CCCTACGAGGGCCGCGTGGAGATACAGCGAGCTGGTGAATGGGGCACCATCTGCGATGAT 216
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                                           3374 CITCCCGCGGCTGGGGGCACCACGACTGCAGGCACAAGGAGGACGCAGGGGTCATCTGCT
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0; Mismatches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/276,400
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EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 09/276,400
EARLIER FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 12
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Best Local Similarity 61.6%;
Matches 173; Conservative
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; ORGANISM: Homo sapiens
US-09-276-400-3
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370 CCCTGGGCTTCGAGAACGCCACCCAGGCTCTGGGCAGAGCTGCCTTCGGGCAAGGATCAG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2285;
                                                                                                                                                                                                                                       APPLICANT: Koths, Kirston E.
APPLICANT: Halenbeck, Robert F.
APPLICANT: Taylor, Eric W.
APPLICANT: Wang, Alice M.
APPLICANT: Casipit, Clayton L.
APPLICANT: Casipit, Secreted Mac-2-Binding Glycoprotein NUMBER OF SECRENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/473,673 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
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les 114;
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llarity 62.1%; Pred. No. 4.4e
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      E: Cetus Oncology Corporation 1400 Fifty-Third Street
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                                                                                                                                                                                 Sequence 9, Application US/08473673 Patent No. 6069127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 29-SEP-1994
APPLICATION NUMBER: US/07/
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Goldman, Kenneth M. REGISTRATION NUMBER: 34,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (510) 420-3152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                          Emeryville
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Best Local Simi
Matches 187;
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US-08-473-673-9
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TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: MNI-073
CURRENT APPLICATION NUMBER: US/09/702,572
CURRENT FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/276,400
                                                                                                                                                  3157 CGCTGTGCCGGGAGAGTAGAGATCTATCACGACGCTTCTGGGGCACCATCTGTGATGAC 3216
                                                                                                                                                                                                         3217 GGCTGGGACCTGAGCGATGCCCACGTGGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTC 3276
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                                                                                                                                                                     Gaps
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                                                                                                DB 4;
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Pred. No. 3.7e-20;
); Mismatches 108;
                                                                                                          ed. No. 3.7e-20,
Mismatches 108;
                                                                                              Score 108.2;
Pred. No. 3.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09702572 Patent No. 6391602 GENERAL INFORMATION:
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                                                                                              2.3%;
Similarity 61.6%;
73; Conservative
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Best Local Similarity 61.6
Matches 173; Conservative
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SOFTWARE: PatentIn Ver. SEQ ID NO 3
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                                                     ORGANISM: Homo sapiens
                         LENGTH: 2262
TYPE: DNA
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TYPE: DNA
                                                                                             Query Match
Best Local Sim
Matches 173;
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US-09-702-572-3
                                                                   US-09-448-076-3
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Sequence 1, Application US/09448076
Patent No. 6300092
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran et al.
TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
FILE REFERENCE: MNI-073CP
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                                                                                                                                             Sequence 1, Application US/09276400
Patent No. 6140056
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: USES THEREFOR
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3397 GACTGCAGGCACAAGGAGGACGCAGGGGTCATCTGCTCAGA 3437
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                        No. 4.3e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 108.2;
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/276,400 CURRENT FILING DATE: 1999-03-25 NUMBER OF SEQ ID NOS: 10 SOFTWARE: PATENTIN VEY. 2.0
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CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/117,580
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 09/276,400
EARLIER FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 12
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Matches 173; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (143)..(2401)
US-09-276-400-1
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                                                                                                                                                                                                                                                                             FILE REFERENCE: MNI-073
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LENGTH: 2920
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US-09-276-400-1
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                                                                                                                                   Gaps
                                                       Ouery Match 2.3%; Score 108.2; DB 4; Length 2920; Best Local Similarity 61.6%; Pred. No. 4.3e-20; Matches 173; Conservative 0; Mismatches 108; Indels 0;
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; NAME/KEY: CDS
; LOCATION: (143)...(2401)
US-09-448-076-1
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Search completed: May 12, 2003, 06:29:49 Job time : 374 secs

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WO200077239-A2
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17141.856 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983_DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985_DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986_DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/
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Maximum Match 100%
Listing first 45 summaries
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. Description	Human TANGO 234 CD	Human TANGO 234 OR	DNA encoding human	Human full-length	Human polynucleoti	Human EST-derived	Human polynucleoti	. Human polynucleoti	Human DNA sequence
ID	AAF45123	AAF45124	AAS01217	AAS44609	AAI58649	AAH98740	AA160435	AA160436	AAS94922
80	22	22	22	22	22	22	22	22	24
% Query Watch Length DB	4628	4359	3670	2800	3716	3834	3834	3834	3707
% Query Match	100.0	94.2	74.8	59.7	31.3	31.3	31.3	31.3	30.5
Score	4628	4359	3459.8	2761.2	1448.2	1448.2	1448.2	1448.2	1409.4
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	2;	1339.2	5.6	3811	7.7	AA158650	polynucleot
	77	8	19.2	4 308	77	AAF45141	WCI ORF
	12	740	•	820	21	AAA43017	secrete
	13	642		069	22	AAH99258	
	14	563		608	20	AAV89272	EST clone CF1:18.
	15	551.4		562	22	AAH99326	Human protein enco
O	16	447.4		449	24	ABL87362	
	17	404		450	22	ABA08369	
	18	379.2		527	22	AAS44781	Human contig polyn
	19	. 335.4		415	22	ABA09428	Human Cys-rich sca
	20	325.8		339	24	ABN24521	Human ORFX polynuc
	21	319.2	6.9	2697	24	AAS17590	DNA encoding novel
	22	213.6		599	20	AAV90288	EST clone DK64: H
	23	213	•	599	20	AAV87660	EST clone DK399.
	24	207.8	4.5	702	21	AAA43661	
	25	199.2	•	461	22	AAK54544	Human haematologic
	26	197.8	4.3	5802	13	AAV49652	
	27	197.6		2562	20	AAX19024	
	28	197.6		3350	20	AAV72589	
	29	193.2		2614	20	AAX19027	
	30	191.6		2376	20	AAV72590	
	31	173.4		444	21	AAC78302	Human cancer assoc
	32	167		474	22	AAH32999	Human colon cancer
	33	162		1269	22	AAD16353	Human sbg14862SPER
	34	149.6	3.2	4344	24	ABK63805	Rat sequence diffe
	35	149.6		4360	18	AAT44068	Rat von Ebner's gl
υ	36	143.8		1165	22	ABA08386	Human M130 antigen
	37	143.6	•	1589	22	AAH33692	
	38	143.2		697	21	AAC99009	pancreatic
	33	140.8	•	29598	13	AAV49654	
	40			1659	22	AAD16354	Human sbg14862SPER
	41	39.	•	28720	19	965	Human SC3 DNA. Ho
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neurological disorder; polar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementla; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety; ss. brain disorder; Gene therapy; TANGO protein; INTERCEPT nervous system; Human TANGO 234 CDNA

21-DEC-2000

24-MAY-2000; 2000WO-US14858.

14-JUN-1999;

(MILL-) MILLENNIUM PHARM INC.

Barnes TM; Sharp JD, Fraser CC, Accarthy SA,

WPI; 2001-032313/04

AAB66037 

useful for of TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful fo screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington' disease

2; 359pp; English. Claim 1; Fig

The present invention relates to TANGO or INVERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66064-B66093 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral solerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder.

Sequence, 4628 BP; 1174 A; 925 C; 1352 G; 1177 T; 0 other;

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ą	1741	ATTGTAACCTGCTCAGGTGATGCAACATGGGGCCTGAGGCTGGTGGGCGGCAACAACCA 1800	_		
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. 4	1801			QQ	2881
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>	1981	AGATGAGATCTCAGATCTCAGGAACAGGAACAGGGGAAATGAGGGAAATGAGAGAAAGAA		οy	3061
; A	1981	TGTGATGGAGATGAGTCAGATCTGTGGAGGAACAGGGGGGGG		. qa	3061
٠,	2041	CAGTGAAGATGTTGGAGTGATCTGTTCTGATGGATGGAATATGGAGGTGAAG 210		ΟŊ	3121
. 8	9			QQ	3121
۵	2101	CTTGTGGGTGGAACCAGGTGTGTGGAAAACGAAAACTTGAGGTGAAACTTGAAGGTGGAAAACTAGAAAAAAAA		οy	3181
, <u>e</u>	2101	CTTGTGGGTGGAAGCAGGTGTGCTGGAAAAGTTGAGGTGAGTGA		qq	3181
>	2161	_	•	δÿ	3241
. A	2,161	GGAATTCTGTGTGCTGAGGCTGGGGAATGAACATTGCTGAAGTTTGCAGCAACTT 2		QQ	3241
>	2221	GAATGTGGGTCTGCAATCAGGGTCTCCAGAGAGCCTCATTCACAGAAAAAAAA	•	, oy	3301
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. >	2281	で、 ROOMERT MET CAN A THE CONTRACT MET CAN A CONTRACT MET		οy	3361
. A	2281			qq	3361
> >	2341	TGGGAGTGGAAACAGACTGCGTGTCATTTAAATATGGAAGTTTGGAAGTTTGGTAACTTCTGCTTCAGCC 240		δλ	3421
g . g	2341		<del></del>	qq	3421
2	2401	CAPAGGCAGCCAGGCTGGTTGGAGCTGATATGCCCTGCTTGGAGGTGAAA 24		δλ	3481
;	2401		-	QQ	3481
. >	2461	CATGCAGACACATGGCGCTCTGTGATTCTGATTCTCTTTTTTTT		QY	3541
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2	2581	A COMPANY TO THE CONTRACT OF T		ΟŊ	3661
, A	2581			qq	3661
	2641	CCATHTATICCOCCATHCHTCAACACCCCAAACACACTHTATATATCCACACACA		δy	3721
; A	2641	CCATTATGCCCCATTGTTCATCTCTCTCTTTTTTTTTCTTCTCTCTC		qq	3721
>	2701	GTTGTCTCTTTTCCCGATATACAGATGTCCGACTTGGAATGGCAAATCCCAGTATGACGGG		Qy	3781
; A	2701	GTIGETCTGTTCCCGATTTACAGATGTCCGACTTCTGAATGCCAAAATCCCAGTGATAAAGCCAAAAAAAA		qq	3781
ج ا	2761	CAACHGGAGATCAACAACGGGGTHTGGACACACHGGGGGTHCACHGGGGGCACCCA S		ΟŊ	3841
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۾	2821	C886 400000000000000000000000000000000000	•	δλ	3901
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GACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCACGCCCAAACCCTGGGGA
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                                                                       TCACTGAATGCCTCCTCAGGTCATTTAGCACTTATTTTATCCAGTATCTTTGGGCTCCTT
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The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB660646-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, partinson's, Gilles de la Tourette's syndrome, neuroposychiatric disorders such as hypertension and sleep disorders, and bipolar affective disorder.
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Best Local Similarity 100.0%;
Matches 4359; Conservative 0
                                   (MILL-) MILLENNIUM PHARM INC.
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                                                                                                                                                                                                                                                               2; 359pp;
                                                                          Fraser
                                                                                                           WPI; 2001-032313/04.
P-PSDB; AAB66037.
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	Y 2788 TGGGGCTCACTGTGACACCCACTGGGACCCAGAAGATGCCCGTGTTCTATGCAGACAG 2847	y 2848 CTCAGCTGTGGGACTGCTCTCAACCACAGGAGAAAATATATTGGAGAAAGAA	2908 CGTGTGTGGGGACACAGGTTTCATTGCTTAGGGGAATGAGTCACTTCTGGATAACTGCTAAA	2881 CGTGTGTGGGGACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAA 2968 ATGACAGTTCTTGGAGCACCTCCTGTATCCATGGAATACTGTCTCTGTGATCTGCCAC  [	SACAGTICTIGGAGCACCTCCTGTATCCATGGAAATACTGTCTCTGTGATCTGCACAAAGCCTGACCTGACCACAGCTGTTTGTCTTGACCTGCAAATGTATCTGACCAAATGTATTTGTCT	3001 GGAAGCCTGACCCACCGCTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTTGTCT 3088 GCAGTTCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGAT	3061 GCAGTTCCAGAGGCCAGTGCTTTGATCTGCTTAGAGGACAACGGCTCCGCCTGGTAGTGGAT 3148 GGGGACAGCCGCTGTGCCGGGAGGAGTAGAGATCTATCACGACGCTTCTGGGGCACCATC	3121 GGGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGCTTCTGGGGGCACCATC 3208 TGTGATGACGGCTGGGACCTGAGCGATGCCCACGTGGTGTGAAAGCTGGGCTGTGA	GTGAT TGGCC TGGCC	2y 3328 GATGACCTGAACTGCACAGGAACGGAGTCCCACTTGTGGCAGTGCCCTTCCCGCGGCTGG 3387	3388 GGGCAGCACGACTGCAGGCACAAGGAGGACGAGGGCTCATCTGCTCAGAATTCACAGGC 3447	3448 T 3421 T	3508 AACGGGACCTGGGGCAGCGTCGGCAGGAACATCACCACAGCCATAGCAGGATTGTG	3481 AACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACCACAGCCATAGCAGGCAG	3541 TGCAGGCAGCTGGGGGGAGAAATGGAGGTTGTCAGCCTCGCCCTTTACTAAAACA 3628 GGCTCTGGTTTCATGTGGGTGGATGACATTCAGTGCCTAAAACGCATATCTCCATATGG	SCTCTGGTTTCATGTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCT AGTGCCTGTCTGCCCCATGGGAGCGAAGAATCTCCAGCCCAGCAGAAGAGA 	3748 ACATGTGA 1111111	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\

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POLY8. POLYX nucleic acids, polypeptides and antibodies to POLYX can be used for treating or preventing a POLYX associated disorder in a subject, preferably a human. These can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from a POLYX-associated disorder, where the therapeutic is a POLYX polypeptide, a POLYX nucleotide or a POLYX antibody. They may also be used to screen for a modulator of activity, or latency, or predisposition to a POLYX associated disorder, e.g. cancer.
                                 POLYX
                                                                                                          secreted
                                 treating or preventing a
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                                                                            English
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                                               disorder, e.g. cancer
                                 useful
                                                                           Page 25-29; 152pp;
                                                                                                         represents the
                                 polypeptide
AAU00396
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898 T; '0'other; Sequence 3670 BP; 947 A; 752 C; 1073 G;

, 8	ery Ma	74.88; SCORE	
രാത	Best Local S Matches 3464	<pre>imilarity 99.8%; Pred. No. 0;  conservative 0; Mismatches 7; In</pre>	0;
	1114	GATGGAGCAGATTTGGAACTGCGACTAGCAGATGGAAGTAACAATTGTTCAGGGAGAGTA 117	73
	200	25	ø.
	1174	GAGGTGAGAATTCATGAACAGTGGTGGACAATATGTGACCAGAACTGGAAGAATGAACAA 123	
	260	31	6
	1234	12	93
	320	GCCCTTGTGTTTGTAAGCAGCTGTTGTTTTTTGCGTCTTTTGCCAGTCGTGTT 379	6
	1294	AAACCTAGTAATGAAGCTAGAGACATTTGGATAAACAGCATATCTTGCACTGGGAATGAG 135	53
	380	43	9
	1354	TCAGCTCTCTGGGACTGCACATATGATGGAAAAGCAAAGCGAACATGCTTCCGAAGATCA 141	13
QQ	440	49	6
	1414	GATGCTGGAGTAATTTGTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGGGCCTCAT 1477	73
	200	GATGCTGGAGTAATTTGTTCTTCTGATAAGGCAGATCTGGACCTAAGGCTTGTCGGGGCTCAT	6
	1474	AGCCCCTGTTATGGGAGATTGGAGGTGAAATACCAAGGAGAGTGGGGGACTGTGTGTT 153	33
	260	61	ō.
	1534	GACAGATGGAGCACAAGGAATGCAGCTGTTGTGTGTAAACAATTGGGATGTGGAAAGCCT 159	693
	620	67	<u>م</u> .
	1594	ATGCATGTGTTTGGTATGACCTATTTTAAAGAAGCATCAGGACCTATTTGGCTGGATGAC 165	53
	089	73	6
	1654	GTTTCTTGCATTGGAAATGAGTCAAATATCTGGGACTGTGAACACAGTGGATGGGGGAAAG 171	13
qq	. 740	79	9
	1714	CATAATTGTGTACACAGAGGGATGTGATTGTAACCTGCTCAGGTGATGCAACATGGGGC 177	73
	800	82	<b>6</b>
	1774	CTGAGGCTGGTGGGCGGCAGCAACCGCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGA 183	133
	860	91	6
	1834	CGGTGGGGCACAGTGTGTGATGACGCTGGAACAGTAAAGCTGCACCTGTGGTGTGTAGC 189	193

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mster; African clawed frog; fruit fly; dog; leukaemia; neuroblastoma; autoimmune disorder; cell proliferation; sorder; inflammatory disorder; cell differentiation; bone regeneration; tendon; ligament; tissue repair; bene regeneration; tendon; ligament; tissue repair; heumatic; antiarthritic; vulherary; antiinflammatory; munosuppressive; vasotropic; antiparkinsonian; osteopathic; antidiabetic; antiparkinsonian; antidiabetic; antiasthmatic; antiallergic; analgesic; gene therapy.
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ပဲ Хu Ren F; Chen R, OA, Ď, Zhao Wang Zhang J, Ma Y, W Asundi V, Zu Zhou P, Asunaı v Wehrman T, Wang Liu C, Yang Y, Tang YT, L Xue AJ, Ya Drmanac R; 

2001-589862/66 WPI; 2001-589862, P-PSDB; AAU27709 olypeptides and nucleic acids obtained from cDNA libraries d from various human tissues, for diagnosis, treatment of neurological, inflammatory disorders and for use in arrays Novel polypeptides and prepared from various hearcer, neurological, i detection

Claim 1; SEQ ID No 34; 153pp; English.

contig polynucleotides encoding polypeptides of the inventions and and protein sequences are useful for the treatment, diagnosis and and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a chuman, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukamia, lymphoma and neuroblastcoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis, disobtes mellitus, allergic thinitis, asthma and eczema, nervous system of disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and disease, ischaemia reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor.

Coll proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to agment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone. cartilage, tendons and ligaments and in tissue répair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. Sequences AAS44576-AAS44919 represent full-length polynucleotides and

Sequence 2800 BP; 697 A; 607 C; 813 G; 683 T; 0 other;

ö 2000 2120 2180 1940 2060 2241 GGTCTCCAGAGAGCCTCATTTCACAGAAAGAACATTACACATCTTAATGTCGAATTCTGG 2300 146 266 326 386 0; Gaps 86 TGTGGTGTGTAGCCAGCTGGACTGCCCATCTTCTATCATTGGCATGGGTCTGGGAACGC CTGGGGAATGAACATTGCTGAAGTTGTTTGCAGGCAACTTGAATGTGGGGTCTGCAATCAG TGTGGTGTGTAGCCAGCTGGACTGCCCATCTTCTATTGGCATGGGTCTGGGAAACGC TCTCTGGTCATGCAGGAACAGTGGGTGGGGAAATAATGACTGCAGTCACAGTGAAGATGT GTGTGCTGGAAAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGGAATTCTGTGTGTAATGG CTGGGGAATGAACATTGCTGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAG GTGACTTTCAGGACGGTGGGGCACAGCGTGTGATGACGGCTGGAACAGTAAAGCTGCAGC TTCTACAGGATATGGAAAAATTTGGCTCGATGATGTTTCCTGTGATGGAGATGAGTCAGA DB 22; Length 2800; Indels 8; Score 2761.2; Pred. No. 0; 0; Mismatches Query Match 59.7%; Best Local Similarity 99.7%; Matches 2766; Conservative 2061 1821 1881 1941 2001 2121 2181 87 147 207 267 327 387 27 a 셤 q g ò ŏ g à ð g ð g ô ò ò

2840 1046 1166 3020 1346 3200 1406 1466 2540 2600 2660 2720 2780 2900 1106 2960 CACCATCTGTGATGACGGCTGGGACCTGAGCGATGCCCACGTGGTGTGTCAAAAGCTGGG 3260 CTGTGGAGTGGCCTTCAATGCCACGGTCTCTGCTCACTTTGGGGAGGGGTCAGGGCCCAT 3320 CIGGCIGGAIGACCIGAACIGCACAGGAACGGAGICCCACIIGIGGCAGIGCCCIICCCG 3380 2420 CTGCACAGGAAGCCTGACCCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATA 1286 926 746 806 866 986 AGTGGATGGGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGG CTGCACAGGAAGCCTGACCCACCACTGTTCCATGCCTCGCAAATGTATCTGACCCATA GTGTCATTTAAATATGGAAGCAAGTTTGATCTGCTCAGGCCCACAGGCAGCCCAGGCTGGT TGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTG TGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTG GGCCGAAAAGTTCCAGTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCA **ACATCCGGAAGACACTTGTATCCACAGCAGAAGTTGGAGTTGTCTGTTCCCGATATAC** AGATGTCCGACTTGTGAATGGCAAATCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCT TGGACACTGGGGCTCACTGTGTGACACCCCACTGGGACCCCAGAAGATGCCCGTGTTCTATG CAGACAGCTCAGCTGTGGGACTGCTCTCTCAACCACGAGGAAAATATTTGGAGAAAG AAGTGTTCGTGTGTGGGGACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAA TITGICIGCAGITCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCT #GGAGCTGATATGCCCTGCTCTGGACGTGTTGAAGTGAAACATGCAGACACATGGCGCTC TGTCTGTGATTCTGATTTCTCTTCTTCTGCTGCCAATGTGCTGTGCAGAGAATTAAATTG 2841 2961 1167 3021 1287 3141 1347 1407 3261 3321 1047 2901 1107 1227 3081 3201 1467 2421 2481 687 2541 747 2601 807 199 867 2721 927 2781 987 2361 627 447 2301 507 267 g QQ Qγ qq g Qγ g δý g Qγ qq δy g ò q δ g οy g δ q Qγ QQ δ g ò g δ pp ò ρp οy ò Ω

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral socierosis, and Shybrager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
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Ku C, Xue AJ,
Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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2000US-0693036.
2000US-0727344.
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P-PSDB; AAM39493.
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Wang Z, F
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09-JUL-2000;
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J, Werhman
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2000US-0617746.
2000US-0631451.
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Drmanac RA,
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P-PSDB; AAM24081.
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                    peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; Huntington's disease; heamostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
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Zhang J
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Yang.Y,
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Xu C, Xue AJ,
Drmanac RT;
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system injuries
                   TGATCTGGACCTAATGAATTCCTCAGGAGGC
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GGACCCACATGGGACAAGAACCTCAGATGAC
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0693036.
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P-PSDB; AAM41279
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25-APR-2000;
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03-AUG-2000;
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19-OCT-2000;
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Wang J,
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Sequence 3834 BP; 979 A; 1082

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Length 3834
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DB 22;
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Score 1448.2;
Pred. No. 0;
31.3%;
65.4%;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's diseases, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
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2289 2498 2229 2558 2169 2618 2109 2678 2049 1989 2858 1869 2978 2709 2198 2438 1809 CCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTTGTCTGCAGTTCCAGA 3098 2018 TGGAGCACCTCCCTGTATCCATGGAAATACTGTCTCTGTGATCTGCACAGGAAGCCTGAC AGGTGCTTCATTATGTCCTTCAGAGCAAGTGGCCTCTGTAATCTGCTCAGGAAACCAGTC TGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCAGAGGCCTCA TTCTCTTTGGGACTGCAAGAACTGGCAATGGGGTGGACTTACCTGTGATCACTATGAAGA TTCTGGACGTGTTGAAGTGAAGCATGCTGACACGTGGGGCTCCATCTGTGATTCGGACTT TTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAGTTCCAGTG TGAAGGGAGTGAAACTCACCTTGCATTATGCCCCCATTGTTCAACATCCGGAAGACACTTG ACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCT AATTTGGCTCGATGATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAA CAGTGGGTGGGGAAATAATGACTGCAGTCACAGTGAAGATGTTGGAGTGATCTGTTCTGA TGCATCGGATATGGAGCTGAGGCTTGTGGGTGGAAGCAGCAGGTGTGCTGGAAAAGTTGA GGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAATGGCTGGGGAATGAACATTGC TGATGTGCTGTTTGCAGGCAGCTGGGATGTGGATCTGCACTCAAAACATCTTATCAAGTGTA TITCACAGAAAGAACAITACACATCTIAAIGICGAAITCIGGCIGCACIGGAGGGGAAGC CTCTCTCTCGGATTGTATACGATGGGAGTGGAAACAGACTGCGTGTCATTTAAATATGGA AGCAAGTTTGATCTGCTCAGCCCACAGGCAGCCCAGGCTGGTTGGAGCTGATATGCCCTG CTCTCTTCATGCTGCCAATGTGCTGTGCAGAGAATTAAATTGTGGAGATGCCATATCTCT GTGTGACACCCCACTGGGACCCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAGCTGTGG GACTGCTCTCTCAACCACAGGAGGAAAATATTGGAGAAAAAAGTGTTCGTGTGTGGG 2648 2408 2559 2048 1988 1928 1808 2079 2468 2348 2439 2288 2499 2228 2168 2619 2108 2739 2799 2859 2919 2768 2019 2708 2139 2588 2199 2528 2319 g ò g g δý Q Οy g qq δý QQ δy g ò g δ g ò Q ò Db ò Dp õ В δy g ŏ g òγ Ω ò qq ò ŏ οy ò

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                                                       CTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCCACCATCTGTGATGACGG
                                                                                                            CTGGGACCTGAGCGATGCCCCACGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGCCTTTCAA
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The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. AASS4746-AASS9021 represent the human polynucleotide sequences of the invention are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development .
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                                                                                                                                  AGGAGAGAACTTAGTCCACCAAATTCAATACCGGGAGATGAATTCTTGCCTGAATGCAGA 432
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TCAGTCATCCTTTATTGCAGTCGGGATCCTTGGGGTTGTTCTGTTGGCCATTTTCGTCGC
                                                       ATTATTCTTCTTGACTAAAAAGCGAAGACACACA--GCGGCTTGCAGTTTCCTCAAG
                                     ATTICICACGIGGIGCCGAGIICAGAAACAAAAACAICIGCCCCICAGAGIITICAACCAG
                                                                                                              AAGGAGGGGTTCTCTCGAGGAGAATTTATTCCATGAGATGGAGACCTGCCTCAAGAGAA
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cardiovascular disorder; coronary artery disease; gene.therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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2675 2795 2855 TCTTGGAGCACCTCCTGTATCCATGGAAATACTGTCTTGTGATCTGCACGGAAGCCT 3035 2495 2555 2615 1726 1606 CTTCTCTCTGGAAGCTGCCAGCGTTCTATGCAGGGAATTACAGTGTGGCACAGTTGTCTC 1666 1907 CCTCTGTAACTCTCACTGGGACATAGAAGATGCCCATGTTCTTTGCCAGCAGCTTAAATG 1966 AAGCCAAAATTACCTGCTCAGGCCCACAGGGAACCCAGACTGGTTGGAGGGGACATTCC TCTTTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCA GGGACACAGGTTTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGT GACCCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTTGTCTGCAGTTCC AGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGATGGGGACAG AGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAATGGCTGGGGÁATGAACATTG AAGCAAGTTTGATCTGCTCAG--CCCACAGGCAGCCCAGGCTGGTTGGAGCTGATATGCC TITCICICITCATGCTGCCAATGTGCTGTGCAGAGAATTAAAATTGTGGAGATGCCATATC GTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAACATCCGGAAGACAC ACTGTGTGTGACACCCACTGGGACCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAGCTG CTGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCAGAGAGCCTC ATTTCACAGAAAGAACATTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGGAAG CCTCTCTCTGGGGATTGTATACGATGGGAGTGGAAACAGACTGCGTGTCATTTAAATATGG GAATGGCAAATCCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCTTGGACACTGGGGCTC 3036 2267 2138 1307 2258 1367 1427 1487 1547 2496 1607 2556 1727 2736 2796 2916 2027 2976 2087 2147 3096 2198 2318 2378 2436 2616 2207 3156 ... Oy g a ç qq qq οy Ω ò 음 ò g ð g g  $\delta \lambda$ Q ΩŽ qq δ a οý qq ò QQ ò qq ŏ g δ οy οy õ g

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                                                                  CTGGGGCAGCGTCGGCAGGAGGAACATCACCACAGCCATAGCAGGCATTGTGTGCAGGCA
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              GAACTGCACAGGAACGGAGTCCCACTTGTGGCAGTGCCCTTCCCGCGGGCTGGGGGCAGCA
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system alseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
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Zhang J;
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Note: The sequence data for this patent did not form part
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Xu C, Xue AJ,
Drmanac RT;
3404 CAGATGATCTGGACCTAATGAATTCCTCAGGAGGC 3438
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Wehrman T, Xu
Goodrich R,
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                                                                                                  AAI58650 standard; cDNA; 3811
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2000US-0552317.
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P-PSDB; AAM39494.
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Wang Z, F
Zhou P,
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Wang J, V
Zhao QA,
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DB 22; Length 3811;

Score 1339.2; Pred. No. 0;

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Query Match Best Local Similarity

Matc	tches 2179; Conservative 0; Mi	smatches 1128; Indels 123; Gaps	s 4;	
1	1002 GCTTGATGGTCTCCTGCTCCGGTAATGAATCTTTTCTTT	1	061 66	
Ч	1062 AACCGTCAATTTTGACTGTCTTCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGC	1	121 .	
-	1122 AGATTTGGAACTGCGACTAGCAGATGGAAGAACAATTGTTCAGGGAGAGTAGAGGTGAG 	1	181 86	
7	1182 AATTCATGAACAGTGGACAATATGTGACCAGAACTGGAAGAATGAACAAGCCCTTGT	3	241 46	
-	1242 GGTTTGTAAGCAGCTAGGATGTCCGTTCAGCGTCTTGGCAGTCGTCGTGCTAAACCTAG 		1301	
П	1302 TAATGAAGCTAGAGACATTTGGATAAACAGCATATCTTGCACTGGGAATGAGTCAGCTCT 	1	361 66	
7	1362 CTGGGACTGCACATATGATGGAAAAGCAAAGCGAACATGCTTCCGAAGATCAGATGC	1	418 26	
7	1419 IGGAGTAATTIGTICIGATAAGGCAGATCIGGACCTAAGGCITGICGGGCICATAGCCC	1	478 86	
7	1479 CTGTTATGGGAGATTGGAGGTGAATACCAAGGAGAGTGGGGGACTGTGTGTCATGACAG 	1	538 46	
	1539 ATGGAGCACAAGGAATGCAGCTGTTGTGTAAACAATTGGGATGTGGAAAGCCTATGCA 	7	598 06	
-	1599 TGTGTTTGGTATGACCTATTTTAAAGAAGCATCAGGACCTATTTGGCTGGATGACGTTTC	7	658 · 66	
-	1659 TTGCATTGGAAATGAGTCAAATATCTGGGACTGTGAACACAGTGGATGGGGAAAGCATAA 	GTGAACACAGTGGGTGGGGAAAGCATAA 17 	718	
-	1719 TTGTACACAGAGAGGTGTGATTGTAACCTGCTCAGGTGATGCAACATGGGGCCTGAG 	GCTCAGGTGATGCAACATGGGGCCTGAG 17'	778 36	
-	1779 GCTGGTGGCGGCAGCAACCGCTGCTGGGAAGACTGGAGGTGTACTTTCAAGGACGTG 	GACTGGAGGTGTACTTTCAAGGACGGTG 18	338 46	
-	1839 GGGCACAGTGTGTGATGACGCTGGAACAGTAAAGCTGCAGCTGTGTGTAGCCAGCT 		1898 1006	
	1899 GGACTGCCCATCTTCTATCATTGGCATGGGTCTGGGAAACGCTTCTACAGGATATGGAAA 		1958 1066	
	1959 ANTITGGCTCGATGATGTTTCCTGTGATGGAGATGAGTCAGTCA	7 7	018 126	
.,	2019 CAGTGGGTGGGGAAATAATGACTGCAGTCACAGTGAAGATGTTGGAGTGATCTGTTCTGA 		2078 1186	

2258 1486 2198 1306 2378 2438 1546 2498 2558 1666 2618 1726 2708 2708 2759 1966 2879 2086 2939 2146 2760 GCAAGTGGAGATCAACGTGCTTGGACACTGGGGGCTCACTGTGTGACACCCCACTGGGACCC 2819 2026 1847 TGGTTCTTATACTGTGAAAGGGACAGGGTTAGGGAGTCATAGCTGTCTTTTTCTAAAGCC 1906 ACCAAAATTACCTGCTCAGCCCACAGGAACCCAGACTGGTTGGAGGGGACATTCCCTG TICTGGACGTGTTGAAGTGAAGCATGGTGACACGTGGGGCTCCATCTGTGATTCGGACTT CTGTCTCCTTCCAGGATACACAGAAATTCGCTTGGTGATGGCAAGACCCCGTGTGAGGG GAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCTTGGAGCACCTCCCTGTATCCA TGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCAGAGAGCCTCA TGATGTGGTTTGCAGGCAGCTGGGATGTGGATCTGCACTCAAAACATCTTATCAAGTGTA AGCAAGTTTGATCTGCTCAGCCCACAGGCAGCCCAGGCTGGTTGGAGCTGATATGCCCTG CTCTCTTCATGCTGCCAATGTGCTGTGCAGAATTAAATTGTGGAGATGCCATATCTCT 2559 TTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCAGTG "-----TTCCCGATATACAGATGTCCGACTTGTGAATGGCAAATCCCAGTGTGACGG AGGAAAATATATTGGAGAAAGAAGTGTTCGTGTGGGGACACAGGTTTCATTGCTTAGG GACTGAGCAGCACATGGGGAGATTGTCCTGTAACTGCTCTAGGTGCTTCATTATGTCCTTC TGCATCGGATATGGAGCTGAGGCTTGTGGGTGGAAGCAGCAGGTGTGTGAAAGTTGA SGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGTTAATGGCTGGGGAATGAACATTGC TTTCACAGAAAGAACATTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGGAAGC CTCTCTCTCGGGATTGTATACGATGGGAGTGGAAACAGACTGCGTGTCATTTAAATATGGA TATCCACAGCAGAGATGGAGTTGTCTG--------. 6612 1367 1547 2499 2820 2880 2087 2940 2079 2139 1247 1307 2259 2319 2379 1487 2439 1607 1667 2619 1727 2679 2709 2709 1907 1961 2027 2147 3000 2207 Db Š. q ò qq qq δ QQ Q δy q. οy qq Óλ qq δy qq δ qq δý Ω οy δ g οy QQ οy g Óγ qq ÓΫ qq ò q ò οy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66046-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder. The present sequence is a sequence used in a sequence homology alignment with the TANGO/INTERCEPT
                                                                                                                                                                                                                                                                                                                                                                                                                   central nervous system; footal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huthington's disease; amyotrophic, lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                        4301
3464 AATTCAATACCGGGAGATGAATTCTTGCCTGAATGCAGATGATCAGGACCTAATGAATTC
                                                                                                          GAATTTATTCCATGAGATGGAGACCTGCCTCAAGAGAGGAGCCCACATGGGACAAGAAC
                                             TCAGAAACAAAAAACATCTGCCCCTCAGAGTTTCAACCAGAAGGAGGGGGTTCTCTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ĭ,
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                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                  4308
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                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                     CDNA;
                                                                                                                                                                                             |||||| | | | CTCAGGAGGC 3533
                                                                                                                                                                        CTCAGATGAC 4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-032313/04.
P-PSDB; AAB66088.
                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                              therapy, TANGO
                                                                                                                                                                                                                                                                                    AAF45141 standard;
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                                                                                                                                                                                                                                                                                                                                                                               Bovine WC1 ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
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AAF45141
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other;

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A; 1093 C; 1410 G; 939

Sequence 4308 BP; 866

present invention

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ŌĂĬ	Query Match 19.2%; Best Local Similarity 54.9%; Matches 2061; Conservative	Score 886.8; DB 22; Length 4308; Pred. No. 1.8e-214; 0; Mismatches 1527; Indels 168; Gap	თ	
Qy Db	483 TCTGGGTTTGAGGCTA             75 TCTGGAGCTGAGGTTG	AACAACTCCTGTTCAGGGAGAGTGGAGGTGAAATT	42 34	
Qy Dp	543 CCAAGAAAGGIGGGGG                 135 CCAAGGAGAAIGGGGC	CCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGAACTTGAATACTGCTGCCGTGGT 60 	602 194	
QY Dp	603 GTGCAGGCAACTAGGA           1  1  195 GTGCAGACAGCTGGGG	GTGCAGGCAACTAGGATGTCCATCTTTTTATTTCTTGGAGTTGTTAATAGCCCTGC 66	662 254	
Qy Dp	663 TGTATTGCGCCCCATTTGGCT 	GGATGACATTTATGCCAGGGGAATGAGTTGGCACTCTG 	722 314	
Oy Op	723 GAÁTTGCAGACATCGT   1    1  315 TGACTGTGAGCATCT	GAÀTIGCAGACAICGIGGAIGGGGAAAICAIGACIGCAGICACAAIGAGGAIGICACAII 78 	82	
Oy Dp	783 AACTTGTTATGATAGT 	AACTIGITAIGATAGTAGTGATCTIGAACTAAGGCTIGTAGGTGGAACTAACGGCTGTAT 84	842 431	
Qy Dp	843 GGGGAGAGTAGAGCTG 	GGGGAGAGTAGAGCTGAAAATCCAAGGAAGGTGGGGSACCGTATGCCACCATAAGTGGAA 90 	902	
Oy Dp	903 CAATGCTGCAGCTGAT           492 ACTTGCCACTGCCCAG	CAATGCTGCAGCTGATGTCGTATGCAAGTGGGATGTGGAACCGCACTTCACTTCGC 96	962 551	
oy Oy	963 IGGCTTGCCTCATITG	TGGCTTGCCTCATTTGCAGTCAGGGTCTGATGTATGGCTTGATGGTGTGTCTCCTGCTC 10 	1022	
Qy Dp	1023 CGGTAATGAATCTTTT	CGGTAATGAATCTTTCTTTGGGACTGCAGACATTCCGGAACCGTCAATTTTGACTGTCT 10 	1082 671	
Qy Db	1083 TCATCAAAACGATGTG 	TCATCAAAACGATGTGTGTGATCTGCTCAGATGGAGCAGATTTGGAACTGCGACTAGC 11 	1142 728	
Qy Dp	1143 AGATGGAAGTAACAAT 	agatggaagtaacaattgttcagggagagtagaggtggaaattcatgaacagtggtggc 12 	1202 788	•
Qy Dp	1203 AATATGTGACCAGAAC               789 GCTCTGTGCCTCCCAC	AATATGTGACCAGAACTGGAAGAATGAACAAGCCCTTGTGGTTTGTAAGCAGCTAGGATG 12	1262	
Qy Dp	1263 TCCGTTCAGCGTCTTT 		1322 908	
Oy Dp	1323 GATAAACAGCATATCT 	GATAAACAGCATATCTTGCACTGGGAATGAGTCAGCTCTCTGGGACTGCACATATGATGG 13	1382 968	
Oy Op	1383 AAAAGCAAAGCGAACA 	AAAAGCAAAGGAACATGCTTCGAAGATCAGATGCTGGAGTAATTTGTTCTGATAAGGC 14	1442 1028	
δ	1443 AGATCTGG	14	450	
qq	1029 GATCCAGGTGCTTCCC	GATCCAGGTGCTTCCCCAGTGCAACGACTCCGTGTCTCAACCTAACAGGCTCTGCGGCCTC 10	1088	

2090 1535 1268 1775 1442 1562 1955 2015 1682 1683 TICTGACCCITGGAATTACAACTCATGCTCTCCAAAGGAGGAAGCCTATATCTGGTG--- 1739 2255 2315 1976 2435 2495 1655 1328 1776 CAGGCTGGTGGGCGCCACCACCGCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGACG 1835 1622 2016 GAACAGTGGGTGGGGAAATAATGACTGCAGTCACAGTGAAGATGTTGGAGTGATCTGTTC 2075 2316 AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAAACAGACTGCGTGTCATTTAAATAT 2375 -- ACCIAAGGCITGTCGGGGCTCATAG 1475 1536 CAGATGGAGCACAAGGAATGCAGCTGTTGTGTAAACAATTGGGATGTGGAAAGCCTAT 1595 1836 GTGGGGCACAGTGTGTGATGACGCTGGAACAGTAAAGCTGCAGCTGTGGTGTGTAGCCA 1895 #GAGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAATGGCTGGGGAATGAACAT 2195 2496 TITCTCTCTTCATGCTGCCAATGTGCTGTGCAGAATTAAATTGTGGAGATGCCATATC 2555 1956 AAAAATTTGGCTCGATGATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAG 1089 AGAGGACAGCGCCCCTACTGCTCAGACAGCAGCTCCGCCTGGTGGACGGGGGCGG 1716 TAATTGTGTACACAGAGGATGTGATTGTAACCTGCTCAGGTGATGCAACATGGGGCCT 1896 (CTGGACTGCCCATCTTCTATCATTGGCATGGGTCTGGGAAACGCTTCTACAGGATATGG 2256 TCATTTCACAGAAGAACATTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGGA 2376 GGAAGCAAGTTTGATCTGCTCAGCCCACAGGCAGCCCAGGCTGGTTGGAGCTGATATGCC 1476 CCCCTGTTATGGGAGATTGGAGGTGAAATACCAAGGAGAGTGGGGGACTGTGTGTCATGA 1596 GCATGTGTTTGGTATGACCTATTTTAAAGAAGCATCAGGACCTATTTGGCTGGATGACGT TICTIGAAGTTIGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCCAGAGAGCC 2196 2436 1451 qq QQ qq Ω g δλ g Οy οp qq Dp qq QY g Óγ QQ δ Q οy qq δ Ω οy Qγ QΩ ΟŻ Óγ  $Q_{\lambda}$ οy δλ qq QΥ QQ δy QQ δy

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2210	2615	2675	2735 2390	2792	2852	2912 2570	2972 2630	3032	3092 2750	3152 2810	3212	3272	3332	3392	3452 3110	3512 3164	3572 3224	3632
111	2556 TCTTTCTGTGGGAGATCACTTTGGAAAAGGGAATGGTCTAACTTGGGCCGAAAAGTTCCA	2616 GTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAACATCCGGAAGACAC	2676 TIGTATCCACAGCAGAAAGTIGGAGTIGTCTGTTCCCGAIATACAGATGTCCGACTTGT	2736 GAATGGCAAATCCCAGTGTGACGGCAAGTGGAGATCAACGTGCTTGGACACTGGGG   1   1   1   1   1   1   1   1   1	2793 CTCACTGTGTGACACCCACTGGGACCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAG	2853 CTGTGGGACTGCTCTCAACCACAGGAAAATATATTGGAGAAAGAA	2913 GIGGGGACACAGGITTCATTGCTTAGGGAATGAGTCACTTCTGGATAACTGTCAAATGAC	2973 AGTICTIGGAGCACCICCTGIAICCAIGGAATACIGICICTGIGAICTGCACAGGAAG	3033 CCTGACCCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCATATTTGTCTGCAGT 1	3093 TCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGATGGGGA	3153 CAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGCCTTCTGGGGCACCATCTGTGA   1   1   1   1   1   1   1   1   1	3213 TGACGGCTGGGACCTGAGCGATGCCCACGTGGTGTGTCAAAAGCTGGGCTGTGGAGTGGC	3273 CITCAATGCCACGGTCTCTGGTCACTTTGGGGAGGGGTCAGGGCCCATCTGGCTGG	3333 CCTGAACTGCACAGGAGTCCCACTTGTGGCAGTGCCCTTCCCGCGGCTGGGGCA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	3393 GCACGACTGCAGGCACAAGGAGGCGCAGGGGTCATCTGCTCAGAATTCACAGCCTTGAG 	3453 GCTCTACAGTGAAACTGAAACAGAGGCTGTGCTGGGAGATTGGAAGTCTTCTATAACGG	3513 GACCTGGGGCAGCGTCGGCAGGAGGAACATCACCACAGCCATAGCAGGCATTGTGTGGGG 1111111111111111111111111111	3573 GCAGCTGGGGGGGGGAGATGTGTCAGCCTCGCCCCTTATCTAAGACAGGCTC
QO	Qy GD	oy P	Qy Db	Qy Db	Qy Db	Oy Dp	Q G	Qy Dp	do do	oy G	Oy Dp	QQ QD	Qy	Qy Dp	Oy Db	Qy Dp	Q P	δŎ,

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Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; hadmatopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiafammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3645 GAGCATCTGGCTGGACGACGACGACGGGGGCCGGGAGTCCTCCCTGTGGACTGTGT 3704
                                                                             3767 --GAGTGCGTGGAGGAGACACCGAGTGCTCTGGGAGAGTGGAGATCTGGCACGCAGGCTC 3824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3825 CTGGGGCACAGTGTGTGATGACTCCTGGGACCTGGCCGAGGCGGAAGTGGTGTGTCAGCA 3884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3945 AACCATCTGGTTGGATGACATGCGGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCA 4004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3225 ACAGCTTGGATGTGGGACAGTGGAAGTCTCAACACTCTGTTGGTCTCAGGGAAGGTTC 3284
                                                                                                                                                           3693 CCTGTCTGCCCCATGGGAGCGAAGTCTCCCAGCCAGAAGAGAGACCTGGATCACATG 3752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4005 CGCCAAACCCTGGGGACAGAGTGACTGTGGACACAAGGAAGATGCTGGCGTGAGGTGCTC 4064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; coaquiation disorder; thempophilia; thrombosis; inflammatory disorder; crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                 3885 GCTGGGCTGTGGCTCTGCTCTGGCTGCCCTGAGGGACGCTTCGTTTGGCCAGGGAACTGG
                                                  3633 IGGTTTCATGTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCTCCATATGGCAGTG
                                                                                                                                                                                                                                                                  3753 TGAAGATAGAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3765 TGGTGTAAGGACATTGCCCACGACCACAGCAGG 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA43017 standard; cDNA; 820 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecules which correspond to the BESTS. Proteins encoded by the BESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coaqulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease). Lumours, bacterial, fungal or viral infections, depression and psoriasis. AAA43420 to AAA43425 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                  Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                 to AAA43419 represent specifically claimed secreted expressed
                                                                                                                                                                                                                                                                                                          Addition to Annually in the control of the control of activities depending on the tissues they were isolated from human, mouse, xenopus and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory, haematopoletic; chemotantic; antibacterial; antifungal; antiviral; antidiabetic; antibacterial; antifungal; antiviral; antidiabetic; antisathmatic; vulnerary; antilicer; osteopathic; neuroprotective; anticonviount; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the identification and isolation of full-length cons.
                                                            ပ်
                                                              Evans
                                                            Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 820 BP; 195 A; 155 C; 233 G; 236 T; 1 other;
                                                            McCoy JM, · LaVallie ER,
                                                                                                                                                                                                                                                       Claim 1; Page 527; 618pp; English.
                 (GEMY ) GENETICS INST INC.
                                                                                Treacy M;
                                                                                                                        WPI; 2000-317937/27
                                                                                  à
                                                            Α,
                                                                                                                                                                                                                                                                                               AAA41261
                                                                                  Merberg
                                                            Jacobs
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5; ACCTTTTCTCTGCTGTGGTAACTTGCATCCTGCTCCTGAATTCCTGCTTTCTCATCAGCA 145 205 264 263 324 323 384 AATGAGTCAGCTCTCTGGGAATGTCAACACCGGGAATGGGGAAGCCATAACTGTTATCAT 444 Gaps TAATGATGCTGCCTCAAAACTCGTGGCATATTGATTTTGGAAGATGCTGCTGTCATCAGA 85 83 TTTGGACAAGCCGTGACTAGACATGGAAAATTTGGCTTGATGTTTTCCTGTTATGGA 24 TAATGATGCTGCCTCAAAACTCGTGGCATATTGATTTTGGAAGATGCTGCTGTCATCAGA GTTTTAATGGAACAGATTTGGAGTTGAGGCTGGTCAATGGAGACGGTCCCTGCTCTGGGA **ACTGCCTCAACTGTCGTGTGCAAACAGCTTGGATGTCCATTTTCTTTTCGCCATGTTTTCGT** 5; Ouery Match
16.0%; Score 740; DB 21; Length 820;
Best Local Similarity 97.2%; Pred. No. 1.5e-177;
Matches 774; Conservative 0; Mismatches 20; Indels 56 84 146 206 325 98 265 264 324 385 g g a ò g ð ð ç aa ö g ò ò

GGAGAAGATGTTGGTGTGAACTGTTATGGTGAAGCCCAATCTGGGTTTGAGGCTAGTGGAT 504

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Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiantiacterial; endocrine; cardiant; central nervous system; virucide; antiafy; fungicide; antimutagen; cardiavascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabethic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic chinitis diabetes; multiple solenosis; depression;
                                                                                                                                                                                                       562
                                                                                                                      622
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                                                                                                                                                                             682
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                                                                                             624
                                        564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                          TGTGATGATGGGTGGAACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCA
                                                                                                                                                    PCTTCTTTTATTTCTTCTGGAGTTGTTAATAGCCCTGCTGTATTGCGCCCCATTTGGCTG
                                                                                                            Human protein encoding cDNA sequence SEQ ID NO:93.
                                                                                                                                                                                                                                                                                                                                                                                                                AAH99258 standard; cDNA; 690 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pang YT, Liu C, Drmanac RT;
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2000US-0488725.
2000US-055317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                     803 CTTGAACGTAGGCTCG 818
                                                                                                                                                                                                                                                                                                                   805 CTTGAACTAAGGCTTG 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease;
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21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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central nervous system; virucide; anti-HV; fungicide; antimutagen; cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary; cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary; antianaemic; antiagregant; haemostatic; vulnerary; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotectides and polynucleotides and polynucleotides and polynucleotides concoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides reserved agonists of a protein and for the treatment and diagnosis; of disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, costeoporosis, severe combined immunodeficiency, eczema, allergic sthankitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
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                                                                                                         AAM959166 to AAM99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1930 CTGGGAAACGCTTCTACAGGATATGGAAAATTTGGCTCGATGATGTTTCCTGTGATGGA 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
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Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 642; DB 22;
Pred. No. 1.1e-152;
); Mismatches 5;
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological disorders.
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Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/Chemofinetic activity, activin/linhibin activity, activity, activity, activin/linhibin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 TAATGATGCTGCCTCAAAACTCGTGGCATATTGATTTTGGAAGATGCTGCTGTCATCAGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 TAATGATGCTGCCTCAAAACTCGTGGCATATTGATTTTGGAAGATGCTGCTGTCATCAGA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy
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2530 GAATTAAATTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGG 2579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merberg
                     640 GAATTAAACTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGG
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Treacy M;
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                                                                                                                               ВР
                                                                                                                               AAV89272 standard; cDNA; 608
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Racie LA, Spaulding V,
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                                                                                                                                                                                                                                                                                                                                     gene therapy; ss
                                                                                                                                                                                                                                           EST clone CF118.
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; central nervous system; virucide; antialized; antimutagen; cardiavascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                        CTGCCTCAACTGTCGTGCAAACAAGAGCTTGGATGTCCA-TTTTCTTTCGCCATGTTTCGT 324
                                                                                     323
                                                                                                              TTTGGACAAGCCGTGACTAGACATGGAAAATTTGGCTTGATGATGTTTCCTGTTATGGA 384
                                                                                                                                                                                                                                                                                                           444
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                                                                                                                                                                                                                                                                                            GGAAACAACTCCTGTTCAGGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGGACTATA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                 GGAGAAGATGTTGGTGTGAACTGTTATGGTGAAGCCAATCTGGGTTTGAGGCTAGTGGAT
                                                                       AATGAGTCAGCTCTCTGGGAATGTCAACACGGGGAATGGGGGAAGCCATAACTGTTATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein encoding cDNA sequence SEQ ID NO:161.
                                                                                                                                                                                                                                                                                                                                                    565 TGTGATGATGGGTGGAACTTGAATACTGCTGCCGT 599
                                                                                                                                                                                                                                                                                                                                                                   BP.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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AAH99326
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AAM25963. The proteins can have antivities based on the fissues and calls they are expressed in, such as: antivities based on the fissues and calls they are expressed in, such as: antivities based on the insulation can his proteins antiather cardiant; central nervous system; virucide; anti-HV; fungicide; antimutagen; cardiavascular; antianaemic; antiagregant; haemostatic; vulnerary; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidapetic; cytostatic; neuroprotective antidepressant; nootropic; antidapetic; cytostatic; neuroprotective antidepressant; nootropic; antidapetic; cytostatic; neuroprotective and polynucleotides are useful for screening for good; production, the proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, reuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, corner, multiple sclerosis, depression, and anemia, platelated discorders, functioned produced produced and confined immunodeficiency, eczema allergic confined immunodeficiency, eczema allergic confined immunodeficiency, eczema allergic confined and 
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                                                       polypeptides, useful for
ulcers and HIV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                       human polynucleotides encoding
                                                                               treatment and diagnosis of e.g. cancer,
                                                                                                                                                                               to AAH99904 encode the human
                                                                                                                               English.
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99.8%;
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Matches 552; Conservative
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P-PSDB; AAM25385
                                                       Isolated
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Search completed: May 12, 2003, 03:08:03 Job time : 683 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Human TANGO 234.	Human TANGO 234 ma	Human TANGO 234 ex	Human secreted pro	Human full-length	Human CD163 recept	Human polypeptide	Human polypeptide	Human polypeptide	Human CD163 recept	
	1 1 1 1 1 1								••		•	
	dī	AAB66037	AAB66039	AAB66040	AAU00396	AAU27709	AAU97585	AAM39493	AAM41279	AAM41280	AAU97584	
	DB	22	22	22	22	22	23	22	22	22	23	
	re Match Length DB I	1453	1413	1319	1120	821	1151	1121	1124	1124	1156	
Query	Match	100.0	97.2	91.3	74.4	55.8	42.3	42.1	42.1	42.1	42.1	
	Score	8138	7913	7426	6058	4540	3441.5	3429	3429	3429	3429	
Result	NO.	1	7	m	4	5	9	7	8	6	10	

WPI; 2001-032313/04. N-PSDB; AAF45123, AAF45124.

CD163 re CD163 re Polypept WC1 pro SRCR pro	Human proctein sequ Rat von Ebner's gl Human proctein sequ Human sbg14862SPER Human serine prote Human neurotrypsin		PRO229 prot angiogenesi PRO 229 prot PRO protein liver celi eptide isola Cys-rich sc lysyl-oxida	Human CG153 (or C5 Murine 1/991 oxtda Human CG153 (or C5 Human 1/991 oxtdas Human secreted pro Human 1/991-oxtdas Human 1/991 oxtdas
AAU9758 AAU9758 AAM3949 AAM5608 AAW6459 AAU0987			22 AAB80227 23 ABB95434 23 ABB84628 23 AAU83648 21 AAB19127 22 ABB12184 23 ABB07650	22 AAE11927 21 AAB00078 22 AAE11935 23 AAG6666 21 AAB12307 23 ABB07653 21 AAB00073
1116 1149 1154 1436 1785 898	225 1290 186 552 422 822 875	143 141 761 761 347	347 347 347 347 757 757	732 754 753 743 641 752 753
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3424 3396.5 3396.5 3082 2435 1763.5	1183 1048.5 1033 971.5 921 822.5	753 719.5 719.5 712.5 691.5	6.11.9 6.01.5 6.01.5 6.34 6.34 6.34	632.5 622.5 622.5 622.5 622.5
11. 11. 11. 11. 11. 11.	17 18 19 20 21 22 23	4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	32 33 34 34 37	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

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central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety.
                                                                                                                                                      protein; INTERCEPT protein; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnes TM;
                              AAB66037 standard; Protein; 1453 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser CC, Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                        24-MAY-2000; 2000WO-US14858
                                                                                         30-MAR-2001 (first entry)
                                                                                                                        Human TANGO 234.
                                                                                                                                                                                                                                                                                           WO200077239-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCarthy SA,
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-1999;
                                                                                                                                                                                                                                                                                                                          21-DEC-2000.
                                                            AAB66037;
                                                                                                                                                      TANGO
RESULT 1
AAB66037
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SCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWG

661

screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's for antibodies, useful and proteins, nucleic acids, and INTERCEPT disease

Fig 2; 359pp; English Claim 8;

sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66064-B66081 and AAB66083. The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders. (CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder. proteins and coding present invention relates to TANGO or INTERCEPT

1453 AA; Sequence

; 0 300 360 360 420 420 480 480 540 540 9 009 099 VEVKFQGQWGTVCDDGWNTTASTVVCKQLGCPFSFAMFRFGQAVTRHGKIWLDDVSCYGN 120 ESALWECQHREWGSHNCYHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTIC 180 Gaps 9 9 QGRWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLW MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLLNSCFLISSFNGTDLELRLVNGDGPCSGT CSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSR RAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVG DDGWNLNTAAVVCRQLGCPSSFISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWG NHDCSHNEDVTLTCYDSSDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVC KOLGCGTALHFAGLPHLOSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVI AHSPCYGRLEVKYQGEWGTVCHDRWSTRNĄAVVCKQLGCGKPMHVFGMTYFKEASGPIWL DDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYF QGRWGTVCDDGWNSKAAAVVCSQLDCPSS11GMGLGNASTGYGKIWLDDVSCDGDESDLW SCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWG Length 1453; .; 0 Indels 22; ; 0 DB Score 8138; Pred. No. 0; Mismatches ; 100.0%; 100.0%; Conservative Local Similarity Matches 1453; Query Match -4 241 301 361 481 541 541 61 61 121 121 181 181 241 301 361 421 421 481 601 601 661 q δ g ò g ŏ g ò 셤 ð g ò 셤 ò g ò g δ 엄 δ g ò ð

1140 780 840 900 MIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKOTACH RLVNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSV RVWGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLS LRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAPLSKT GSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGGDTECSGRVE IWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNES FLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKSLNASSGHLALILSSIFGLLLLVLFILFL TWCRVQKQKHLPLRVSTRRRGSLEENLFHEMETCLKREDPHGTRTSDDTPNHGCEDASDT VAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTA LNMEASLICSAHROPRLYGADMPCSGRVEVKHADTWRSYCDSDFSLHAANVLCRELNCGD AISLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDV MNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACH AA AAB66039 standard; Protein; 1413 SLLGVLPASEATK AAB66039; 1261 1381 1021 1081 1141 1201 1261 1321 1321 1381 1441 1441 781 1021 1201 721 721 781 841 901 901 961 961 RESULT qq QQ δλ pp q Вb δλ δλ g δλ q δy qq δ g δλ δ Ω g a ŏ δy ò

234 mature protein. (first entry) 30-MAR-2001 Human TANGO AAB66039 

TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety.

sapiens Homo

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KPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDAT
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Pred. No. 0;
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                                                                                                                                      Barnes TM;
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                                                                                                                                      Sharp JD,
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100.0%; Pre-
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         WO200077239-A2
                                                            24-MAY-2000;
                                                                                                                                     McCarthy SA,
                                                                                    14-JUN-1999;
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TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebroyascular; Alrahemer's disease; senile dementia; Huntington's disease; amyotrophic lateral solerosis; parkinson's, Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66064-B66033 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzhelmer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder.
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extracellular domain
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Mammal, human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster: African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimnume disorder; cell prolliferation; nervous system disorder; inflammatory disorder; cell differentiation; anglogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiarthritic; vulnerary; antinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;
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                                                                                                                                                                                                                                                                                                                    GEMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGGDTECSGRVEIW
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                                                                                                                             510 SLYGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRL
                                                                                                                                                                           903 VNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRV
                                                                                                                                                                                           WGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAV
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                                                                                                                                                                                                                                                                                                                                                   FL;
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                                                              human;
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                                                              protein; therapeutic; diagnostic;
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Pred. No. 0;
0; Mismatches
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99US-0154520.
99US-0154762.
99US-0159231.
2000US-0659634.
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llarity 99.7%;
Conservative
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(first entry)
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Best Local Similarity
Matches 1088; Conserv
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                               Human secreted
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16-SEP-1999;
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04-JUL-2001
                                                                                                                                                         22-MAR-2001
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181 ADTWRSVCDSDFSLHAANVLCRELNCGDAISLSVGDHFGKGNGLTWAEKFQCEGSETHLA
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22-FEB-2001; 2001US-270120P.
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                                                                                                                                                                                                                                                                                                                             Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for detection
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                                                                                                                                                                                                                                                Xu C;
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Chen P
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, Wang D,
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Ma Y,
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r, Wang J,
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Xue AJ, Yang Y, Wehrman T,
                                                                                                                  2000US-0515126.
2000US-0577409.
2000US-0597707.
2000US-0616807.
2000US-064641.
                                                                                       26-FEB-2001; 2001WO-US04926
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                                                                                                                                 18-MAY-2000;
17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
     Homo sapiens.
                                                                                                                   28-FEB-2000;
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les 820;
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Human; CD163; receptor; haptoglobin-haemoglobin complex; Hp-Hb complex; CD163 receptor variant; antibiotic; anticancer drug; anti-HIV drug; human immunodeficiency virus; haemolysis; haematological condition; aplastic anaemia; iron-deficiency anaemia; megaloblastic anaemia; sickle-cell anaemia; polycythaemia; malaria; leukaemia; myelodysplasia; lymphoma; leucopenia; splenectomia; inflammation; infection; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmunity; immunodeficiency; CD163 receptor extracellular variant
                                  481 WQCPSRGWGQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1173 TTAIAGIVCRQLGCGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSAPWERRIS
LCPIVQHPEDTCIHSREVGVVCSRYTDVRLVNGKSQCDGQVEINVLGHWGSLCDTHWDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CD163 receptor extracellular variant protein sequence.
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401 EADVVCRQLGCGSALKTSYQVYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHY 460

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New haptoglobin-haemoglobin complex or its mimics or receptors, useful in gene therapy, particularly for treating an individual suffering from e.g. haemolysis, anaemia, inflammation, infection, cancer or autoimmunity
                                                                                              present invention relates to a new haptoglobin-haemoglobin (Hp-Hb)
                                                                               Claim 1; Fig 5; 70pp; English.
(PROT-) PROTEOPHARMA APS
              Moller HJ;
              Moestrup S,
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complex, or its part or maine; being operably linked to a substance, capable of binding a CD163 receptor and/or a CD163 receptor variant.

The HP-HP complex or its maine; her CD163 variant or the CD163 receptor are useful as a medicament or in the manufacture of a medicament for are useful as a medicament or in the manufacture of a medicament for treating an individual. The medicament comprises at least one drug to be delivered to a cell expressing a CD163 receptor or a CD163 variant. The continuous and an anticancer drug, e.g. an anti-HIV (human continuous) drug, e.g. an anti-HIV (human continuous) drug, e.g. an anti-HIV (human continuous) drug, the CD163 variant or the medicament are immunodeficlency virus) drug. In particular, the HP-Hb complex or its minic, the CD163 variant or the CD163 variant or the medicament are coseful for treating haemolysis and/or other haematological conditions, applastic anaemia, iron-deficiency anaemia, megaloblastic anaemia, caplastic anaemia, polycythaemia, malaria, leukaemia, myelodysplasia, lumpon a leucopenia, splenectomia, inflammation, infection, cancer, cautoimmunity or immunodeficiency. The medicament of an individual. The medicament is also useful for inhibiting (in vivo) uptake of haemogloblo in in cells presenting a CD163 variant is also useful in a presenting and/or controlling a condition in an individual. Controlling a condition in an individual. Controlling a condition in an individual. The complex in serum and/or plasma of an individual. The present amino acid sequence represents the human CD163 receptor represents and prove the present and or the invention.

DB 23; Length 1151; 42.3%; Score 3441.5; DB 23 ilarity 55.2%; Pred. No. 2.7e-239; Conservative 166; Mismatches 311; 1151 AA; Local Similarity nes 608; Conserv Seguence Query Match Best Loca Matches

; è 221 LICNGNESALMNCKHQGWGKHNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQG 280 542 220 602 PSNEARDIWINSISCTGNESALWDCTYDGKAKRT-CFRRSDAGVICSDKADLDLRLVGAH SSAGSGRIWMDHVSCRGNESALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGG GADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAK SPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDD VSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQG RWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSC 364 424 101 191 603 281 483 g οg 8 q ð g ò ò οy ò

40200153312-A1.

IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN 782

RNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMN 722

663 341 723

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26-JUL-2001

STATEMENT STATEM WGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAV 1022 FNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTALR 1142 LYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAPLSKTGS 1202 .203 GFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGGDTECSGRVEIW 1262 HAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL 1322 WDCHAKPWGQSDCGHKEDAGVRCSGQSLK----SLNASSGHLALILSSIFGLLLLVLF 1376 I - - LFLTWCRVQKQKHLPLRVSTRRRGSLEENLFHEMETCLKREDPHGTRTSDDTPNHGC 1434 peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; 461 EEAKITCSAHREPRLVGGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV VNGK SQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRV PEGSALICLEDKRLRLVDGDSRCAGRVE1YHDGFWGTICDDGWDLSDAHVVCQKLGCGVA SLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRL cytostatic; gene therapy; nootropic; immunosuppressant; Ą AAM39493 standard; Protein; 1121 EDASDISLIGV --- LPASEATK 1453 ADFSAAELISVSKFLPISGMEK 1137 polypeptide SEQ ID NO (first entry) 22-OCT-2001 AAM39493; Human 701 1143 1263 1001 1377 843 903 1023 881 1435 521 963 1061 RESULT 7 AAM39493 ò g g g δ g ŏ δŽ g ò QQ δ qq δ QQ δλ 8 δy pp οy g οχ QΥ

us-09-759-130b-381.rag

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723 IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN
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                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                             useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 GADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSAGSGRIWMDHVSCRGNESALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMCSGRIEIKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 VSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 LICHGNESALWACKHQGWGKHNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMN
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                                                                                                                                                                                                                                                     Ren F, W
Zhang J;
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'Yang Y,
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Best Local Similarity 56.2%; Pred. No. 2.1e-238;
Matches 598; Conservative 161; Mismatches 294;
                                                                                                                                                                                                                                                     Chen R, Ma Y, C
Xu C, Xue AJ,
, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                  system injuries
                                                                                                                                                                                                                                                                                                                                                                               nucleic acids and polypeptides,
                                                                                                                                                                                                                                                       Chen
                                                                                                                                                                                                                                                     Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                         2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                     2000US-0552317.
                    2000WO-US34263
                                                      2000US-0488725
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                                                                                                                                                                                                                                                                                                                                                                                                  such as central nervous
                                                                                                                                                                                                                                                                                                                         WPI; 2001-442253/47.
N-PSDB; AAI58649.
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                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                         03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                  26-DEC-2000;
                                                                                                          19-JUL-2000;
                                                                                          09-JUL-2000;
                                                                                                                                                                                                                                                   Tang YT,
Wang J, V
Zhao QA,
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                                                                                           903 VNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRV
                                                                                                                                                                                                                                                                                                                                                           WGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAV
                                                                                                                                                                                                                                                                                                                                                                                       646 WRHMFHCTGTEQHMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPTRPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDCHAKPWGQSDCGHKEDAGVRCSGQSLK----SLNASSGHLALILSSIFGLLLLVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1006 WDCPARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIAVGILGVVLLAIF
                                                                                                                                                               SLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRL
                                                                                                                                                                                                                                                                                       1023 PEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1083 FNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCROLGCGENGVVSLAPLSKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1203 GFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGGDTECSGRVEIW
MEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I -- LFLTWCRVQKQKHLPLRVSTRRGSLEENLFHEMETCLKRED 1419
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGGSWGTVCDDSWDLDDAQVVCQQLGCGPALKAFKEAEFGQGTGFIWLNEVKCKGNESSL 1008
EADVVCRQLGCGSALKTSYQVYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHY 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYIDVRL
                                                                                                                            VNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRV
                                                                                                                                                                                                                                                          WCHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAV
                                                                                                                                                                                                                                                                                                                                 1023 PEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVA
                                                                                                                                                                                                                                                                                                                                                    FNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAPLSKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1203 GFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGDTECSGRVEIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        889 IPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEETWITCDNKIRLQEGPTSCSGRVEIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL
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                                                                                                                                                                                                                                                                                            WRHMFHCTGTEQHMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPTRPTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as lateral schenois, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constants.
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                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries :
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Zhang J;
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Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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                 2000US-0488725.
2000US-0552317.
2000US-0598042.
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2000US-0662191.
2000US-0693036.
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29-NOV-2000; 2000US-0727344
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Zhou P,
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Wang 2,
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                                  25-APR-2000;
09-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                       Wang
                                                                                                                                                                                                                                                       polypeptides, useful for treating disorders system injuries -
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Zhang J;
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Yang Y,
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Local Similarity 56.2%; Pred. No. 2.1e-238;
es 598; Conservative 161; Mismatches 294;
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u C, Xue AJ,
Drmanac RT;
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                 20000S-0598042.
20000S-0620312.
20000S-0653450.
20000S-0662191.
20000S-0693036.
                                                                                                                                                    Liu C, Asundi V,
Wang Z, Wehrman T,
Zhou P, Goodrich R
      2000US-0552317
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29-NOV-2000;
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                                  19-JUL-2000;
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sickle-cell anaemia; polycythaemia; malaria; leukaemia; myelodysplasia; lymphoma; leucopenia; splenectomia; inflammation; infection; cancer; autoimmunity; immunodeficiency; CD163 receptor cytoplasmic variant 2.
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                                                                                                                                                                                           1263 HAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDCHAKPWGQSDCGHKEDAGVRCSGQSLK----SLNASSGHLALILSSIFGLLLLVLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1203 GFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGGDTECSGRVEIW
                                                                                                                                                                                                                                                                                         1143 LYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCROLGCGENGVVSLAPLSKTGS
                                                                        SLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRL
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2001DK-0000039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aplastic anaemia, incondeficiency anaemia, megalobiastic anaemia, sickle-cell anaemia, polycythaemia, malaria, leukaemia, myelodysplasia, lymphoma, leucopenia, splenectomia, inflammation, infection, cancer, autoimmunity or immunodeficiency. The method involves drug-delivery treatment of an individual. The medicament is also useful for inhibiting (in vivo) uptake of haemoglobin in cells presenting a CD163 receptor. The CD163 variant is also useful in diagnosing, monitoring and/or controlling a condition in an individual. In particular, the CD163 variant is useful for identifying macrophages in a blological sample from an individual, for identifying at least one Hp-Hb complex in serum and/or plasma of an individual, or for removing at least one Hp-Hb complex in serum and/or plasma of an individual. The present amino acid sequence represents the human CD163 receptor cytoplasmic variant 2 of the invention.
                                                                                                                               New haptoglobin-haemoglobin complex or its mimics or receptors, useful in gene therapy, particularly for treating an individual suffering from e.g. haemolysis, anaemia, inflammation, infection, cancer or autoimmunity
                                                                                                                                                                                                                                                                complex, or its part or mints, being operably linked to a substance, capable of binding a CD163 receptor and/or a CD163 receptor variant. The Hp-Hb complex or its mints, the CD163 variant or the CD163 receptor variant are useful as a medicament or in the manufacture of a medicament for treating an individual. The medicament comprises at least one drug to be delivered to a cell expressing a CD163 receptor or a CD163 variant. The medicament may also comprise at least one gene to be delivered to a cell expressing a CD163 variant. The medicament is an antiblotic or an anticancer drug, e.g. an anti-HIV (human anticancer drug, e.g. an anti-HIV (human immunodeficiency virus) drug. In particular, the Hp-Hb complex or its minic, the CD163 variant or the CD163 receptor, or the medicament are useful for treating haemolysis and/or other haematological conditions,
                                                                                                                                                                                                                                                      a new haptoglobin-haemoglobin (Hp-Hb)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 PSNEARDIWINSISCTGNESALWDCTYDGKAKRT-CFRRSDAGVICSDKADLDLRLVGAH 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSC.662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEAŞGPIWLDD
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Pred. No. 2.2e-238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598; Conservative 161; Mismatches
                                                                                                                                                                                                                                                      invention relates to
                                                                                                                                                                                                                     5; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.1%;
22-FEB-2001; 2001US-270120P.
                                  (PROT-) PROTEOPHARMA APS.
                                                                Moller HJ;
                                                                                                WPI; 2002-452380/48
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                                                                                                                                                                                                                     Claim 1; Fig
                                                                  Moestrup S,
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Human; CD163; receptor; haptoglobin-haemoglobin complex; Hp-Hb complex; CD163 receptor variant; antibiotic; anticancer drug; anti-HIV drug; human immunodeficiency virus; haemolysis; haematological condition; aplastic anaemia; iron-deficiency anaemia; megalobiastic anaemia; sickle-cell anaemia; polycythaemia; malaria; leukaemia; myelodysplasia; lymphcma; leucopenia; splenectomia; inflammation; infection; cancer;
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                                                                                                                                                                                                                    962
                                                                                                                                            HAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL
723 IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN
                                                                                         VNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRV
                                                                                                                                                                                                                                       WGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAV
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                                   BADVVCRQLGCGSALKTSYQVYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHY
                                                                      783 MEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAI
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/note= "Specifically claimed in claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CD163 receptor protein sequence.
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Domain
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sickle-cell anaemia, polycythemia, megalorasir, disemia, angeliasia, sickle-cell anaemia, polycythemia, medalatia, leukaemia, myelodysplasia, lymphoma, leucopenia, splenectomia, inflammation, infection, cancer, autoimmunity or immunodeficiency. The method involves drug-delivery treatment or gene delivery treatment of an individual. The medicament is also useful for inhibiting (in vivo) uptake of haemoglobin in cells presenting a CDIG3 receptor. The CDIG3 variant is also useful in diagnosing, monitoring and/or controlling a condition in an individual. In particular, the CDIG3 variant is useful for identifying macrophages in a blodogical sample from an individual, for identifying at least one Hp-Hb complex in serum and/or plasma of an individual, or for removing at least one hp-Hb complex in serum and/or plasma of an individual. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New haptoglobin-haemoglobin complex or its mimics or receptors, useful in gene therapy, particularly for treating an individual suffering from e.g. haemolysis, anaemia, inflammation, infection, cancer or autoimmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex, or its part or minic, being operably linked to a substance, capable of binding a CD163 receptor and/or a CD163 receptor variant. The HP-HB complex or its minic, the CD163 variant or the CD163 receptor are useful as a medicament or in the manufacture of a medicament for treating an individual. The medicament comprises at least one drug to be delivered to a cell expressing a CD163 receptor or a CD163 variant. The medicament may also comprise at least one gene to be delivered to a cell expressing a CD163 variant. The medicament is an antibiotic or an anticancer drug, e.g. an anti-HIV (human is an antibiotic or an anticancer drug, e.g. an anti-HIV (human is an antibiotic or an anticancer drug, in particular, the HP-HB complex or its minic, the CD163 variant or the CD163 receptor, or the medicament are useful for treating haemolysis and/or other haematological conditions, aplastic anaemia, iron-deficiency anaemia, megaloblastic anaemia,
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                                                                                   claim 6"
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/note= "Specifically claimed in claim 6"
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/label- Domain_9
/note= "Specifically claimed in claim
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368.467
/label= Domain_4
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/note= "Specifically
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2001DK-0000039.
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1262
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receptor of the
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                                                                                                                 364 GADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAK 423
                                                                                                                                        GIDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAVSVICNQLGCPTAIKAPGWAN 100
                                                                                                                                                                  PSNEARDIWINSISCTGNESALWDCTYDGKAKRT-CFRRSDAGVICSDKADLDLRLVGAH 482
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                                                                                         Gaps
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                                                                                                                                                                                                                                  281 EWGTICDDGWDSYDAAVACKQLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQC
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                                                                                                                                                                                                                    SPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDD
                                                                                                                                                                                                                                                                        543 VSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQG
                                                                                                                                                                                                                                                                                                                        603 RWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSC
                                                                                         12;
                                                                 Length 1116;
                                                                                        Indels
 present amino acid sequence represents the human CD163
                                                              Query Match 42.1%; Score 3424; DB 23; Best Local Similarity 56.1%; Pred. No. 4.8e-238; Matches 597; Conservative 161; Mismatches 295;
                                        1116 AA;
              invention
                                         Sequence
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New haptoglobin-haemoglobin complex or its mimics or receptors, useful in gene therapy, particularly for treating an individual suffering from e.g. haemolysis, anaemia, inflammation, infection, cancer or autoimmunity
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The Hp-Hb complex or its mimic, the CD163 variant or the CD163 receptor are useful as a medicament or in the manufacture of a medicament for treating an individual. The medicament comprises at least one drug to be delivered to a cell expressing a CD163 receptor or a CD163 variant. The medicament may also comprise at least one gene to be delivered to a cell expressing a CD163 receptor or a CD163 variant. The medicament is an antibolic or an anticancer drug, e.g. an anti-HIV (human immunodeficiency virus) drug. In particular, the Hp-Hb complex or its mimic, the CD163 variant or the CD163 receptor, or the medicament are useful for treating haemolysis and/or other haematological conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sickle-cell anaemia, polycythaemia, malaria, leukaemia, myelodysplasia, tymphoma, Leucopenia, splenectomia, inflammation, infection, cancer, autoimmunity or immunodeficiency. The method involves drug-delivery treatment or gene delivery treatment of an individual. The medicament is also useful for inhibiting (in vivo) uptake of haemoglobin in cells presenting a CD163 receptor. The CD163 variant is also useful in diagnosing, monitoring and/or controlling a condition in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sickle-cell anaemia; polycythaemia; malaria; leukaemia; myelodysplasia; lymphoma; leucopenia; splenectomia; inflammation; infection; cancer; autoimmunity; immunodeficiency; CD163 receptor cytoplasmic variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complex;
WDCHAKPWGQSDCGHKEDAGVRCSGQSLK----SLNASSGHLALILSSIFGLLLLVLF 1376
                                                                     WDCPARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIAVGILGVVLLAIF 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; CD163; receptor; haptoglobin-haemoglobin complex; Hp-Hb complex CD163 receptor variant; antiblotic; anticancer drug; anti-HJV drug; human immunodeficiency virus; haemolysis; haematological condition; aplastic anaemia; iron-deficiency anaemia; megalobiastic anaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CD163 receptor cytoplasmic variant 1 protein sequence.
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11-JAN-2001; 2001bK-0000039.
22-FEB-2001; 2001US-270120P.
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In particular, the CD163 variant is useful for identifying macrophages in a biological sample from an individual, for identifying at least one Hp-Hb complex in serum and/or plasma of an individual, or for removing at least one Hp-Hb complex in serum and/or plasma of an individual. The present amino acid sequence represents the human CD163 receptor
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Pred. No. 4.8e-236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathses and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
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                                                                                           RISSPAEETWITCEDRIRVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGC 1289
                                                                                                                                                                                                                                                                                 nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                           peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating disorders
             GSALAALRDASFGQGTGTIWLDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQS
                                                                                 LK-----SLNASSGHLALILSSIFGLLLLVLFI--LFLTWCRVQKQKHLPLRVSTRRRG
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Zhang J
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Yang Y,
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Xue AJ,
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Drmanac RT;
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                                                                                                                                                                                                AAM39494 standard; Protein; 1154
                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 2639.
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0620312.
2000US-0653450.
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1118 LVHQIQYREMNSCLNADD 1135
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2000US-0693036.
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2000US-0552317
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                                                                                                                          SLEENLFHEMETCLKRED
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N-PSDB; AAI58650.
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens,
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19-JUL-2000;
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29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                     leukaemia.
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Zhao QA,
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lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                        The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNITTAIAGIVCRQLGCGENGVVSLAPLSKTGSGFWWVDDIQCPKTHISIWQCLSAPWER 1229
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                                                                                                                                                                                                                                                   Length 1154,
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                                                                                                                                                                                                                                                                                               295; Indels
                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                Ouery Match

41.7%; Score 3396.5; DB 2;
Best Local Similarity 54.4%; Pred. No. 4.8e-236;
Matches 597; Conservative 161; Mismatches 295;
                                                                                                                                                                                                           1154 AA;
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sedneuces
                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                            Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; creebrovscular; Alzheimer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F43136 and AAF45138-F45139 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders, such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychlatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder. The present sequence is a sequence used in a sequence homology alignment with the TANGO/INTERCEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                              1349
                                                                                                      1065
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                                                                                                                                                       1066 VQKTPQKATTGRSSRQSSFIAVGILGVVLLAIFVALFFLTKKRRQRQR---LAVSSRGEN 1122
                                                                                       SSMSETTVGVVCRQLGCADKGKINPASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEK
                                        RISSPAEETWITCEDRIRVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGC
                                                                           GSALAALRDASFGQGTGTIWLDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .LRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHNCRHKQDAGVICS--EFLALRMVSEDQQCAGWLEVFYNGTWGSVCRNPMEDITVSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQLECGSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLSVGDHFGKGNGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQLDCPSSIIGMGLGNAST - - - GYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATVSSFFGTGSGPIWLDEVNCRGEESQVWRCPSWGWRQHNCNHQEDAGVICSGF--VRL
                                                                                                                                  Indels 154;
                                                                                   Length 1436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOILTARFHCSGAESFLWSCPVTALGGPDCSHGNTASVICSGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                Conservative 208; Mismatches 495;
                                                                                                           3.1e-213;
                                                                                      Score 3082;
                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
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of the present invention
                                                                                      37.98;
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                                         1436 AA;
                                                                                                           Similarity
                                                                                                                                  613;
                                            Sequence
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### ### ##############################
MSCEVPLAGEDOCSHGARTS/TCGGSHTQVLDQCNDFLSQPAGSASESSPYCSDSRQL RILDDLAGGGRUETHUGGWGTTCDDCWDLSDAHVVCQKLCCCVAFNATVSAHFGEGSG RILLII
<b>10</b>

28; a human protein which contains a SRCR (scavenger domain. The gene and encoded protein can be used nours, particularly of the nervous system ona) or breast. The DNA sequence and probes d to identify genes that express SRCR-domain determine the form in which these proteins exist icance of individual forms on cellular can be used to detect the presence of odies which regulate its expression. EVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTY 530 GSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDCPS 628 | :|| || || :|| :|| || || || || || s GGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGGGW 668 SQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAG 848 DIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSD 470 SDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNIAEV 726 TERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLNMEAS 786 SGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLS 845 AVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTL 252 HFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFD 350 SAPGNARFGQGSGPIVLDDVRCSGYESYLWSCPHNGWLSHN 451 RLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQL 410 ODVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICS---- 683 VIGIRLYDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVV 192 -----DSSDLELRLVGGTNRCMGRVELKIQGRWGTVCHHK 290 Gaps :VEVKFQGQWGTVCDDGWNTTASTVVCKQLGCPFSFAM--- 97 SNIWDCEHSGWGKHNCVHREDVIVTCSGDA-----TW-9%; Score 2435; DB 19; Length 1785; 1%; Pred. No. 1.9e-166; 155; Mismatches 415; Indels 374; YGNESALWECOHREWGSHNCYHGEDVGVNCY---

867	905	986	965	946	1023	1006	1083	1059	1143	1116	1166	1174	1196	1234	1255.	1267	1315	1327			
							DGWDLSDAHVVCQKLGCGVAF												352	364	
	846 VGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLVNG	:    :     SRASTAGSESTLAL	INVLGHWGSLCDTHWDPEDARVLCRQLSCG	GDRCKGRVEVLYQGSWGTVCDDYWDINDANVVCRQLGCGWAMSAPGNAQFGQGSGPIVLD	LLDNCOMTVLGAPPCIHGNTVSVICTGSLT	DVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSAAQSQSTPRPDTWLTINLPALTVGS	DKRLRLVDGDSRCAGRVEIYHDGFWGTICD	ESSLALRLVNGGDRCRGRVEVLYRGSWGTVCDDSWDTNDANVVCRQLGCGWAM	NATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTALR	GCSGPIVLDDVRCSGNESYLWSCPHKGWLT	YSETETESCAGRLEVFY-NGTWGS	PTTTTARPSSNCGGFL - FYASGTFSSPS	VGRRNIAD	KLEAHHNCSFDYVEIFDGSLNSSLLLGKIC	WVDDIQCPKTHISIWQCLSAPWERRISSP	ISFQNTGFLAWINRLVNLNSSYGLC	SSWGTVCDDSWDLAEAEVVCQQLGCGSALA	AGRVEIYHGGTWGTVCDDSWTIQEAEVVCRQLGCGRAVSALGNAYFGSGSGPITLDDVBC	KGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKS 1352	CRNRGWFSHNCNHREDAGVICSGNHLST 1	
:     :    849 VICSASQSQP	VGDHFGKGN		KSQCDGQVE	GDRCRGRVE	RFHCLGNES	DVRCSGHES	EGSALICLE	ESSL	NATVSAHFG	SAPGNARFG	YSET	NSTTTDWWH	VGRRNI	RINLGFSNL	LSKTGSGFM	ISFQNTGFL		AGRVEIYHG	KGNESFLWD	SGTESTLWO	
849	846	898	906	887	996	947	1024	1007	1084	1060	1144	1117	1167	1175	1197	1235	1256	1268	1316	1328	
qq	δλ	qq	Οy	Q	ογ	q	Qy	QQ	ογ	Ω	ογ	qq	Οy	QQ	Οy	qq	οy	QQ	οy	QQ	

Search completed: May 12, 2003, 06:37:17 Job time : 63 secs



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GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on:

May 12, 2003, 06.29:56; Search time 33 Seconds

(without alignments)
4232.828 Million cell updates/sec

Title:
Perfect score: 8138
Sequence: 1 MMLPQNSWHIDFGRCCCHQN......CEDASDTSLLGVLPASEATK 1453
Scoring table: BLOSUM62
Scoring table: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224
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lse: PIR\_73:\*

1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

RIES	Description	M130 antigen	antigen	antigen	~		scavenger receptor	scavenger receptor	hensin - rabbit	CRP-ductin-alpha p		ebnerin precursor	scavenger receptor	brain-specific ser	scavenger receptor	- wscde precursor	T-cell glycoprotei	speract receptor p	mucin (clone pGM31	cyclophilin C-asso	Mac-2-binding glyc	. macrophage bacteri	macrophage scaveng	lymphocyte surface	esin - mc	T-cell surface gly				
SUMMARIES	ΩI	138004	138005	138006	A46496	A59386	T14893	T18524	T30549	T42721	S56744	A57190	T17405	JC5759	JC4361	149100	S26741	A32751	S56745	A53202	A47161	A55840	B44407	A38415	S08276	146862	A44407	A29079	T42215	A26396
	DB	7	7	~	7	7	~	~	7	~	~	~	~	ď	~	~	~	7	7	7	7	~	7	~	~	7	7	-	~	-
	Query Match Length	1151	1156	1149	1436	2403	2153	2043	1594	2083	900	1290	1036	761	918	626	468	532	504	577	585	518	458	451	453	454	454	494	5376	495
dР	Query	42.3	42.1	41.7	37.9	36.7	30.0	27.6	26.5	24.1	13.2			8.9	8.2	7.7	7.3	6.4	4.7	3.9	3.8	3.6	3.6	m.	3.4		m		3.2	3.1
	Score	3441.5	3429	3396.5	3082	2990	2439.5	2246.5	2156.5	1962.5	1076.5	1048.5	866.5	720.5	665	626.5	594.5	520	385	314.5	311.5	290.5	290	288	279.5	279.5	273.5	264	'n	254.5
	Result No.	П	2	e	4	S	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	. 27	28	29

cell-fate determin . Notch-1 protein -	fibrillin-1 precur MEGF6 protein – ra	alpha-2-macroglobu notch protein homo	T-cell surface gly	. notch homolog - se	Balbian1 ring 3 pr	Notch homolog prot	fibrillin 1 precur	notch protein - fr	fibrillin I - bovi	alpha-2-macroglobu	flbrillin-2 precur	T-cell surface gly.
A49128 A46019	A55624 T13954	S02392 S18188	543536	T31070	S08167	T30201	A47221	A24420	A55567	S25111	A57278	S11270
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0.0	3.0 9.0	2.9	2.9	5.9	5.9	5.9	2.8	2.8	2.8	2.8	2.8	2.7
246.5 3.0 2	244.5 3.0 240 2.9	239.5 2.9	235 2.9	234 2.9	233 2.9	232 2.9	231.5 2.8	230 2.8	230 2.8	224.5 2.8	224 2.8	223.5 2.7

## ALIGNMENTS

RESULT 1  138004  Millo antigen precursor, splice form 3 - human  C.Species: Homo sapiens (man)  C.Species: John	F.41-1045/Domain: actracellular #status predicted <pre>F.41-1045/Domain: actracellular #status predicted <pre>F.41-1045/Domain: actracellular #status predicted <pre>F.43-147/Domain: acavenger receptor cysteine-rich domain homology <src1> F.151-244/Domain: scavenger receptor cysteine-rich domain homology <src2> F.365-468/Domain: scavenger receptor cysteine-rich domain homology <src4> F.365-468/Domain: scavenger receptor cysteine-rich domain homology <src4> F.375-678/Domain: scavenger receptor cysteine-rich domain homology <src6> F.711-814/Domain: scavenger receptor cysteine-rich domain homology <src6> F.311-814/Domain: scavenger receptor cysteine-rich domain homology <src6> F.311-814/Domain: scavenger receptor cysteine-rich domain homology <src8> F.311-814/Domain: scavenger receptor cysteine-rich domain homology <src8> F.311-814/Domain: intracellular #status predicted <irn> F.301-1024/Domain: intracellular #status predicted <irn> F.301-1024/Domain: intracellular #status predicted <irn> F.301-1024/Domain: intracellular #status predicted <irn> F.301-1034/Domain: intracellular #status #status</irn></irn></irn></irn></irn></irn></irn></irn></irn></irn></irn></irn></irn></irn></irn></irn></src8></src8></src6></src6></src6></src4></src4></src2></src1></pre></pre></pre>
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                                                                                                                    RNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMN 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1061 VALFFLTKKRRQRQR---LAVSSRGENLVHQIQYREMNSCLNADDLDLMNSSEN--SHES
                                                                                                                                                                                                                                                                                                                                                       PEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVA
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                                                                                        IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN
                                                                                                                                                                     MEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAI
SPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDD
                                       RWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSC
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M130 antigen precursor, splice form 4 - human N;Alternate names: M130 antigen cytosolic variant

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A;Note: the locus has not been clearly established and like to some contrained in the constrainty; scavenger receptor cysteine-rich domain homology cysteyords: alternative splicing; glycoprotein; surface antigen; transmembrane protein cysteyords: alternative splicing; glycoprotein; surface antigen; transmembrane protein cysteyords: alternative splicing; glycoprotein; surface antigen; transmembrane protein cysteine-rich domain homology cysteine-rich dom
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                                                                                                                                A.Tricle: A new macrophage differentiation antigen which is a member of the scavenger A.Reference number: 138003; MUID:93380506; PMID:8370408
                                                                                           Y.; Willis, A.C.; Mason,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Asn) (covalent)
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                                                                                                                                                                                                                                                   A)Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Molecule type: GLAWA
A); Residues: 1.1156 CLAWA
A); Cross-references: EMBL: Z22970; NID: 9312145; PIDN: CAA80543.1; PID: 9312146
C); Comment: For other splice forms, see PIR: 134004 and PIR: 134006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 GADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAK 423
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C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_c;
C;Accession: 138065; S36079
R;Law, S. K.; Micklem, K.J.; Shaw, J.M.; Zhang, X.P.; Dong,
Eur. J. Immunol. 23, 2320-2325, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:M130; GDB:MM130
A;Cross-references: GDB:119369; OMIM:133710; GDB:99
A;Map position: 10pter-110qter
A;Note: the locus has not been clearly established
                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
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A. Map position: lopter-10qter
A. Map position: lopter-10qter
A. Mote: the locus has not been clearly established and there is some confusion in the a C. Superfamily: scavenger receptor cysteine-rich domain homology
C. Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein F:140-7Domain: signal sequence #status predicted <SIG>F:41-1149/Product: M130 antigen, splice form 1 #status predicted <MATI>F:41-11078/Domain: extracellular #status predicted <EXT>
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A) Status: preliminary: translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A) Residues: 1-1149 < LAM1>
A) Cross-references: EMBL: 222971; NID: 9312147; PIDN: CAA80544.1; PID: 9312148
A) Accession: 138003
A) Actus: preliminary; translated from GB/EMBL/DDBJ
A) Molecule type: mRNA
A) Residues: 1-573, "R, 608-1149 < LAM2>
C) Comment: For other splice forms, see PIR: 134004 and PIR: 134005.
                                                                                                                                                                                                                                                                           WGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAV 1022
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F;955-1057/Domain: scavenger receptor cysteine-rich domain homology <SRC9> F;1079-1095/Domain: transmembrane #status predicted <TRN> F;100-1105/Domain: intracellular #status predicted <INT> F;1100-1118,226,315,440,713,722,795,1029/Binding site: carbohydrate (Asn) (covalent) #s ŝ predicted 1049 1109 SHLWQCPSRGWGQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGR 1169 760 340 400 880 580 929 640 700 602 722 IAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLN 782 F;41-573,'F',608-1149/Product: M130 antigen, splice form 2 #status predict F;43-147/Domain: scavenger receptor cysteine-rich domain homology <SRC1>F;151-254/Domain: scavenger receptor cysteine-rich domain homology <SRC2>F;256-361/Tomain: scavenger receptor cysteine-rich domain homology <SRC3>F;365-468/Domain: scavenger receptor cysteine-rich domain homology <SRC4>F;470-573/Tomain: scavenger receptor cysteine-rich domain homology <SRC5>F;608-711/Tomain: scavenger receptor cysteine-rich domain homology <SRC5>F;444-847/Tomain: scavenger receptor cysteine-rich domain homology <SRC5>F;449-954/Tomain: scavenger receptor cysteine-rich domain homology <SRC5>F;849-954/Tomain: scavenger receptor cysteine-rich domain homology <SRC8>F;849-954/Tomain: scavenger receptor cysteine-rich domain homology <SRC8>F;849-954/Tomain scavenger receptor cysteine-rich domain homology <SRC8>F;849-954/Tomain scavenger receptor cysteine-rich domain homology <SRC8>F;840-954/Tomain scavenger receptor cysteine-rich domain homology <SRC8-F;840 281 EWGTICDDGWDSYDAAVACKQLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQC PSNEARDIWINSISCTGNESALWDCTYDGKAKRT-CFRRSDAGVICSDKADLDLRLVGAH SAGSGRIWMDHVSCRGNESALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGG LIGSYTVKGTGLGSHSCLFLKPCLLPGYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHW 364 GADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAK SPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDD 543 VSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQG RNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMN -----TDDVRLVNGKSQCDGQVEINVLGHWGSLCDTHW DPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGNESLLDNCOMTVLGAPPC IHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRCAGRV EIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGEGSGPIWLDDLNCTGTE FWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSC EADVVCRQLGCGSALKTSYQVYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHY SLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSR-----DB 2; Length 1149; Indels 295; Pred. No. 1.7e-212; 41.7%; Score 3396.5; 54.4%; Pred. No. 1.7e Conservative 161; Mismatches

HODERINGADANCALIMINING HIM DINICAL MEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	म व्य	QY 142 DVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSS 201	QY 202 FISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDSSDLE 261	QY 262 LRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGS 321   :     :     :     :	OY 322 DVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICSDGADLELRLADGSNNCSGR 381	QY 382 VEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAKPSNEARDIWINSISCTGN 441 ::::   :::   :::	OY 442 ESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVGAHSPCYGRLEVKYQGEWGTVC 501	QY 502 HDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWG 561 DD 1	QY 562 KHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVC 621 11 11 11 11 11 11 11 11 11 11 11 11 1	QY 622 SQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSED 677	OY 678 VGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQLECGSAI 737  DD 576 AYIWCADSRQIRLVDGGGRCSGRVEILDQGSWGTICDDRWDLDDARVVCKQLGCGEAL 633	QY 738 RVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLNMEASLICSAHRQPRL 797 :	OY 798 VGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLSVGDHFGKGNGLT 857   1   1   1   1   1   1   1   1   1	QY 858 WAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLV-NGKSQCDGQVEIN 916	OY 917 VLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGNESLL 976 :     :     :     :	QY 977 DNCOMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRL 1036 1	OY 1037 RLVDGDSRCAGRVEIXHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGEGSG 1096 11111	QY 1097 PIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTALRLYSETETESCAGRL 1156	Qy 1157 EVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAPLSKTGSGFMWVDDIQCPKTH 1216
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PRSC SALA SALA CLPT VSTR VSTR ALSS	<pre>veveGressognE 1372 an) nce_revision 31-Dec-2001 #text_change 31-Dec-2001 equence Database, March 2001</pre>	cd. No. 9.2e-186; Mismatches 504; Indels 230; Gaps 23 GTVCDDGWNTTASTVCKOLGCPFSFAMFRF 100         :     :      :	FGGGSGPIVLDDVRCSGHESYLMSCPNNGWLSHNCGHHEDAGVICSAAQSRSTPRPDTLS 706
	RESULT 5 A59366 sanko - human C; Species: Homo saplens (man) C; Date: 31-Dec-2001 #sequence_revision 3; C; Accession: A59386 R; sanko, S. submitted to the Protein Sequence Databa: A; Reference number: A59386 A; Accession: A59386 A; Accession: A59386 A; Accession: A59386 A; Molecule type: protein A; Residues: 1-2403 <san></san>	16.7%; Local Similarity 40.5%; Local Conservative 17 Local	FGGGSGPIVLDDVRCSG
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g Q	470	DKADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGC 5	519
Οy	C	KPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCS	
qq	767	:	826
Οy	577	RLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAA	617
go,	827	STAGSESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDSWDTSDA	988
οy	618	MGLGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSED	677
qq	887	CRELGCGWATSAPGNARFGQGSGPIVLDDVRCSGYESYLWSCPHNGWLSHNCQHSED	946
δλ	678	SDMELRLVGGSSRCAGKVEVNVQGAVGI	713
qq	947	VGSESSLALRLVNGGDRCOGRVEVLYOGS	1000
δλ	714		773
QQ	1007	NARFGGGSGPIVLDDVRCSGHESYLWSCPHNG	106
οy	774	-QPRLVGADMPCSGRVE	809
Dp	1067	PSPDTWPTSHASTAGSESSLALRLVNGGDRCQGRVE	112(
οy	810	NGLTWAEKFOCEGSET	698
qq	1127	NDANVVCRQLGCGWAMSAPGNARFGQGSGPIVLDDVRCSGHES	1186
οy	870	VRLVNG	905
qq	1187	STATELLA STATES STATES STATES STATES STATE STATES STATES STATE STATES ST	124
οy	906	DOCOVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGH	965
-Q	1247	GCGWATSAPGNARFGQGSGPIVLD	130(
δy	996	GENERALIDINCOMTVLGAPPCIHGNTVSVICTGSLTOPLFPCLANVSDPYLSAVPEG	102
g	1307	H H H H SPYLWSCPHNGWLSHNCGHHEDAGVICSASQSQPT-PSPDTWPTSHASTAGSE	136
٥y	1026	ALICLEDKRLRLVDGDSRCAGRVETYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNA	108
g	1366	ALRLYNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWATSA	141
δλ	1086	GEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVIC	113
QQ	1420	ARFGQGSGPIALDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQPTPS	147
Qy	1136	SEFT-ALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVC	118
QQ	1480	GSWGTVCDDYWDTNDANVVC	153
Qγ	1182	QLGCGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSAPW	122
qq	1538	CGWAMSAPGNAQFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDA	159
οy	1228	SSPAEETWITCEDRIRVRGGDTECSGRVEIWHAGSWGT	126
QQ	1595	SQSTPRPDTWLTTNLPALTVGSESSLALRLVNGGD-RCRGRVEVLYRGSWGT	165
Οý	1270	STGTIWLDDMRCKGNESFLWDCHAKP	1329
Op	1654	CDDSWDTNDANVVCRQLGCGWAMSAPGNARFGQGSGPIVLDDVRCSGNESYLWSCPHKG	171
δλ	1330	WQQSDCGHKEDAGVRCSGQSLKSLNASSGH 1359	
qq	1714	WLTHNCGHHEDAGVICSATOINSTITDWWH 1743	

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                                            scavenger receptor cysteine-rich protein precursor - sea urchin (Strongylocentrotus pu C; Species: Strongylocentrotus purple urchin)
C; Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C; Accession: T14893
R; Pancer, Z.; Rast, J.P.; Davidson, E.H.
Immunogenetics 49, 773-786, 1999
A; Title: Origins of immunity: transcription factors and homologs of effector genes of A; Reference number: 218253; MUID:99328904; PMID:10398804
                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                  A;Residues: 1-2153 <PAN>
A;Cross-references: EMBL:AF064259; NID:g4165052; PID:g4165053; PIDN:AAD08654.1
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                                                                                                                                                                                                                                                                                                                                                                                                         113 LSSCAYVSSHNCAHSEDAGVVCAGSGDGNIRLVGGSHSSEGRVELYVNNQWGTVCDDLWD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAKP--SNEARDIWIN 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWGNNDCSHSEDVGVICSDASD -- MELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNI 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTASTVVCKQLGC-PFSFAMFRFGQAVTRHGKIWLDDVSCYGNESALWECQHREWGSHNC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHGEDVGVNCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLG 197
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                  ----GIDLELRLVNGDGPCSGTVEVKFQGQWGTVCDDGWN 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 GHSEDAGVICSSRFGSDIRVVGGSIPTEGRVEVFVNGAWGTVCDDLWDINDASVACRQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 LSSDIRVVGGRSPTEGRVEVFVNRAWGTVCDDLWDVNDTNVACRQLGFGRAISAPGGASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 KYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNDAQVACRQLGLGPAVSADAHFGEG ---SGSILLDNVACIGTETSLLSCSHPGIESHNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 CPSSFISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVILTCYDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 SISCTGNESALWDCTYDGKAKRTCFRRSDAGVIC---SDKADLDLRLVGAHSPCYGRLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 NVGCSGNERSLELCSNNGIGVHNCGHQEDASVVCTGVTTMPGMNIRIVGGGSPSEGRVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 IWDCEHSGWGKHNCVHREDVIVTCSGDATWG-----LRLVGGSNRCSGRLEVYFQGRWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    606 TVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 FGRAISASGGASYGQGSGSIFLDNLACTGAESNLLSCPHNGVGSHNCGHGEDAGVLCSSS
                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                   Length 2153;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                 Query Match 30.0%; Score 2439.5; DB 2; Best Local Similarity 38.2%; Pred. No. 4.3e-150; Matches 527; Conservative 197; Mismatches 560;
                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ: Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                    LNSCFLISSFN-----
                                                                                                                                                                                   A; Accession: T14893
                                                                                                                                                                                                                                                                                     A; Gene: SRCR12
                                                                                                                                                                                                                                                                    Genetics
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C;Genetics:
A;Gene: SRCRM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHSSFFGPGRGDILLDDVSCTGSEDDILDC---SHPPIGTNNCGHSEDAGVVCD--LN 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Geodia cydonium
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 885
                                                                                 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWHIDEGRCCCHONLESAVVTCILLINSCFLISSFNGTDLELRLV-NGDGPCSGTVEVKF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scavenger receptor cysteine-rich protein homolog srcrm2 - Geodia cydonium
                                                                                                                                                                                                                                                                                                                  AHVVCRQLGFGPALSAVTAASFGQGSGSILMDNVQCSGDEATIAECSHNGIGIHNCGHQE
                                                                                                                                                                                                                               1080 GVAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1140 ALRL---YSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1208 TIRLAGGRSKXE----GRVEILQNGAMGTVCDNQMDVHDAAVVCRELGYATTLEATSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1197 LSKTGSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVR--GGDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1315 CKGNESFLWDCHAKPWGQSDCGHKEDAGVRC----SGQSLKSLNASSGHLALILSSIF
                                        EASLICS-AHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAI
                                                                  SLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHP - - - EDTCIHSREVGVVCSRYTD
                                                                                                                                                                                                         900 VRLVNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERS
                                                                                                                                                                                                                                                                                           960 VRVWGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYL
                                                                                                                                                                                                                                                                                                                                                                            1020 SAVPEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2043
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<u>&gt;</u>	9 ,	~	
ð	157	ADEWGSICDDYFGFGEAVVICHELGFPSAEDSHGGGTFPQGDGLIWMDNLQCTGHESSIA 216	
<u>≯</u> ₽	126	ECQHREWGSHNCYHGEDVGVNCYGEANLGLRLYDGNNSCSGRVEVKFQ 173	
<u>≻</u> 9	174	ERWGTICDDGWNLNTAAVVCRQLGCPSSFISSGVVNSPAVLRPIWLDDILCQGNELA 230	
<u>⊁</u> q	231	LWNCRHRGWGNHDCSHNEDVTLTCYDSSDLELRLVGGTNRCMGRVEL 277	
<u>≯</u>	278	KIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVWLDGVSCSGNESF 33	
۵	396		
<u>⊁</u>	338	LWDCRHSGTVNFDCLHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWMTIC 394 :	,
٠ ج	395	DONWKNEOALVVCKOLGCPFSVFGSRRAKPSNEARDIWINSISCTGNESALMDC	
<u>و</u>	514	DDSWGAEDAQVICHQLGFYGTATAVRGTQFGFASSSQPIWLDDVGCTGSEMYLSDC 56	
. a	570	SSSGFGNHNCYHYEDAGVVCQGTSFAIPVRLSNGTRPNGGTVEIFYQNRWGTICDIFWTL 629	
Δ	469		
ą	630	YDANVVCRQLGYDGAYNATHSSYYGDSGLTTVTAYTDCFGQESQLANCTGFRYPYIPSW 689	
<u>~</u>	469		
ð	069		
<b>≿</b> ₽	515	KQLG-CGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIMDCEHSGWGKHNCVHREDVIV 573 :1   :       :                RQLGYLSEGATALQFAHFGEGSGPIVLDDVNCTGLELYVTDCPSSGFYIHNCAHSEDAGV 809	
<i></i> ≿	574	TCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLD 62	
ą	810		
ჯ გ	626 869	CPSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLMSCRNSGWGNNDCSHSE 676	
λ	677		
ą	921	QAGVACTNYTASEYPIRLYGGSGPHEGRVEIYYGGVWGTVCDDSWGQPDADVVCRQLGYA 980	
<u> </u>	735	SAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLNWEASLICSAHRQ 794	,
ă	186	NASRATVRAEFGRGTGEIWLDNVACTGFENSLDECRSNGWGDHNCGHREDAGAVCQGELL 104	9
≿ g	795	P-RLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLSVGDHFGKG 853	0
	854		
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ą	1161		0
⋩	996	RFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEG 1025	Ŋ

g	1221	: ::::  :
Qy	1026	SALICLED
qa	1261	LRLVNGNTEGEGRVEVFHRGSWGTVCDDHWSEIDANIVCKELGFARAISA 1310
Qy Db	1086	TVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTAL 1141 :
λo :	1142	RLYSETETESCAGRLEVFYNGTWGSVGRRNİTTAIAGIVCRQLGC-GENGVVSLAPLSKT 120
a g	1371	QLIDGPSVHEGRLQIYYNNEWGTVCDDQWGYDEANVVCKSLGFPGADPDNSLLNSYGP
do O	1429	CSGHIWLDDVDCRGDEFFIQDCNHADIGENNCGHYEDVGLRCLPTTL
δy	1258	
qq	1489	
0γ	1317	
QO	1549	GYEDSLLECSHAGVKVHNCRHSEDASVVCS
Qy	1377	ILFLTWCRVQKQKHLPLRVSTRRG 1401
RES T30 D ben C;S C;D	ULT 8 549 sin - 1 pecies ate: 2; ccessic	RESULT 8 T30549 hensin - rabbit C; Species: Ortcolagus cuniculus (domestic rabbit) C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C; Accession: T30549
H . H &	akito, Clin. itle: 1 eference	J.: Hikita, C.: Al-Awqati, Q. Invest. 98, 2324-2331, 1996 Hensin, a new collecting duct protein involved in the in vitro plasticity of ce number: 220851; MUID:97096804; PMID:8941650 .
A A A	ccessic tatus: olecule	on: T30549 preliminary; translated from GB/EMBL/DDBJ e type: mRNA
A;R A;C	esidue ross-r	s: 1-1594 <tak> eferences: EMBL:AF043112; NID:g4105083; PID:g4105084; PIDN:AAD02242.1</tak>
OME	Query Ma Best Loc Matches	y Match 26.5%; Score 2156.5; DB 2; Length 1594; Local Similarity 36.6%; Pred. No. 7.1e-132; hes 475; Conservative 132; Mismatches 387; Indels 303; Gaps 29;
ΟŊ	46	
QΩ	51	
0y	103	AVIRHGKIWLDDVSCYGNESALWECQHREWGSHNCYHGEDVGVNCYG149
qq	111	
Qy	150	
qq	168	
Qy Db	191	VYCRQLGCPSSFISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDC 244           :
ογ	245	
QQ	282	. :     :   GROWDTTTPPPDTWPTTVIYESSPVFPSGLELRLANGSDRCQGRVEVLYQ 341
Qy	281	GRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWD 340

qq	342 GS	:	
δλ	341 CI	RHSGTVNFDCLHQNDVSVICSDGADLELRLADGSN 376	
qq	402 CI	: :	
Qy	377 NG 	NCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAKPSNEARDIWINSI 436	
Oy Op	437 SC   519 SC	SCTGNESALWDCTYDGKAKRTCFRRSDAGVICSD	
ζQ.	473 DI 579 GI	DLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFK 532 	
Qy Db	533 E/2 : 639 QC	EASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDATW 581	
Z qa	582 - V 699 V	GLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDCPS 628 	
δ, O	629 S	SIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVIGSDA-SD 687 ::	
ογ Op	688 M	MELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTE 747 : :      :    :    :   :  :  :  :	
3 % A			
QY	ø 0		
λο qα	m 10		
Qy Dp	910 p	CDTHWDP  : CN	
Qy Dp	970 Ld 1039 -	LGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALI 1029	
Qy Bp	1030 C	CLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNAT 1086 	
QY		VSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGOHDCRHKEDAGVICSEFTA 1140  :                  :   :   :	-
QY	1141 L 1181 P	LRLYSETETESCAGRLEVFYNGTWGSVGR 1169 : : :	
RES T42 CRP C;S	ULT 9 721 -ductin- pecies:	RESULT 9 T42771 CRP-ductin-alpha precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 23-Mar-2001	

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Anat. Rec. 244, 327-343, 1996
Anat. Reference number: 222241; MUID:96362470; PMID:8742698
Ancession: T42721

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 DGTDSGLAVRLVNGGDRCQGRVEILYQGSWGTVCDDSWDLNDANVVCRQLGCGLAVSAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 -FREGQAVTRHGKIWLDDVSCYGNESALWECQHREWGSHNCYHGEDVGVNCYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EANLGLRLVDGNNSCSGRVEVKFQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 RWGTICDDGWNLNTAAVVCRQLG------CPSSFISSGVVNSPAVLRPIWLDDILCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 ---SDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 ALVVCKQLGCPFSVFGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- DKADLDLRLVGAHSPCYGRLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.1%; Score 1962.5; DB 2; Length 2083; llarity 28.9%; Pred. No. 3.7e-119; Conservative 164; Mismatches 503; Indels 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STGYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICSDA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 497; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAGVICS----
C; Accession: T42721
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i		
g	796 GQGTGPIVMDDVACGGYEDYLMRCSHRGWLSHNCGHHEDAGVICSASQSSSPTPDVFYPT 855	A: Molecule type: mRNA
ογ	686SDMELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNIAEV 726	A; Residues: 1-600 < NUN>
qq	856 DQTTVEQTTVPDYTPIGTENSLAVRLENGGDRCQGRVEILYQGSWGTVCDDSWDTKDANV 915	A; Cross-reterences: GB:S
ογ	727 VCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLNMEAS 786	F:11-102/Domain: scavenger
Q	916 VCRQLGCGWAVSAPGNAYFGPGSGSIVLDDVACTGHEDYLWSCSHRGWLSHNCGHHEDAG 975	F;380-483/Domain: scaven
ογ	787 LICSAHRQPRL 806	Query Match
qq	:    ; :     ; :       ; :      ; :      ; :      ; :      ; :      ; :      ; :      ; :      ; :      ; :	Best Local Similarity Matches 223; Conserv
ò	807RVEVKHADTWROEVKHADTW	Qy 48 LRLVNGDGPCSGTV
Q		Db 2 LRLVNGSDRCQGRVI
ογ	821 DSDFSLHAANVLCRELNCGDAISLSVGDHFGKGNG 855	Qy 105 TRHGKIWLDDVSCY
Ор	1096 DGSNGSFTSTGNFMSVVFITDGSVTRRGFQAHYYSTVSTGCGLLTQPSGQFSSPXYP 1155	Db 61SGPIVLDDVGCS
ŏ	856 LTWAEKFOCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLVNGKSO 908	Qy 148YG-EANLGLRLVI
qq	: :      :         :         :	Db 119 TDYGTESGLALRLV
δ	909CDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIG 956	Qy 205 SGVVNS-PAVLR
qq	1199 GPQYNSSLIARVCDGSNGSFTSTGNFMSVVFIT 1231	Db 173 -GWANSAPGNARFG
δ	957 ERSVRVWGHRFHCLGNESLLDNCQMTVLGAPPCIHGNTVSVICTGSLTQP 1006	Qy 255rbs
QQ	1232 DGSVTRRGEGAHYYSTVSTTPPVPIPTTDDYSCGGLLTLPSGQFSSPHYP 1281	Db 232 QTQSTVVPDLMYPT
ΟŊ	1007	Qy 298 VVCKQLGCGTALHF
qq	1282 SNYPNNARCSWEILVPNWNRVTVAFTDVQLEGGCNYDYIL-VYDGPEYN 1329	
ογ	VSAHFGEGSGPIWLDDLNCT GT	Qy 358 SVICSDGADLELRL
q	1330 SSLIARVCDGSNGSFTSTGNFMSVVFITDGSVIRRGFQAH 1369	Db 352 SVICSA
δ	1112 LWQCPSRGWGQHDCRHKEDAGVICS1136	Qy 418 GSRRAKPSNEARDI
qq	1370 YYSTVYTUXSCGGLLTQPSGQFSSPHYPSNYPNNVRCSWEILVPSMNRVTVAFTDVQLEG 1429	707 366 da
οy	1137 EFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGE 1188	QY 478 LVGAHSPCYGRLEVI
qq	1430 GCSFDYILVYDGPEXNSSLIAPVCDGFNGSFTSTGNFMS1468	Db 385 LVNGSDRCQGRVEV
ογ	1189 NGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDR 1245	QY 538 IMLDDVSCIGNESN
QQ	1469VVFITDGSVTRRGF	Db 445 ILLDDVGCSGYETY
Οy	1246 IRVRGCDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGGGGSALAALRDASFGQGT 1305	
QQ	1508 LRLVNGSNRCEGRVEILYRGSWGTVCDDSWGISDANVVCRQLGCGSALSAPGNAWFGQGS 1567	
ογ	CKGNESFLWDCHAKPWGQSDCGH	C; Species: Rattus norved
qq	1568 GLIVLDDVSCSGYESHLWNCHHPGWLVHNCRHSEDAGVICA 1608	C;Date: IU-NOV-1995 #Seq C;Accession: A57190 R:Li X I Shyder S H
11000	OF EL	J. Biol. Chem. 270, 1767

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é
mucin (clone pGM7-1) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 20-Apr-2000
C;Accession: S5674
R;Nunes, D.P.; Keates, A.C.; Afdhal, N.H.; Offner, G.D.
Bjochem J. 310, 41-48, 1995
A;Title: Bovine gall-bladder mucin contains two distinct tandem repeating sequences: A;Reference number: S56744; MUID:95374471; PMID:7646470
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A.Molecule Lype: mRNA
A;Residues: 1-1290 <LLA>
A;Cross_references: GB:U32681; NID:g975346; PIDN:AAC52248.1; PID:g975347
C;Superfamily: scavenger receptor cysteine-rich domain homology; Clr/Cls repeat homol
C;Reywords: extracellular protein; transmembrane protein
C;Keywords: extracellular protein; cysteine-rich domain homology #status atypical <SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ţ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Natus norvegicus (Norway rat)
C.Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C.Baccession: A57190
R.Li, X.J.; Snyder, S.H.
J. Biol. Chem. 270, 17674-17679, 1995
A.Title: Molecular cloning of Ebnerin, a von Ebner's gland protein associated with the Reference number: A57190; MUID:9535352; PMID:7629065
                                                                       <SRC1>
                                                                                                                                                                                                                                                                                       13;
("Cross-references: GB:S78981, NID:g1042036; PIDN:AAB35069.1; PID:g1042037; Superfamily: scavenger receptor cysteine-rich domain homology (fragment): 1.126-229/Domain: scavenger receptor cysteine-rich domain homology (fragment): 1.25-3.356/Domain: scavenger receptor cysteine-rich domain homology cSRC2> 3.53-3356/Domain: scavenger receptor cysteine-rich domain homology cSRC3> 3.80-483/Domain: scavenger receptor cysteine-rich domain homology cSRC3> 3.80-483/Domain: scavenger receptor cysteine-rich domain homology cSRC4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365
                                                                                                                                                                                                                      13.2%; Score 1076.5; DB 2; Length 600; 38.5%; Pred. No. 2.9e-62; Live 52; Mismatches 157; Indels 147; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 TRHGKIWLDDVSCYGNESALWECQHREWGSHNCYHGEDVGVNC-------147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --YG-EANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSSFIS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVVNS-PAVLR-----PIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTC--- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 -GWANSAPGNARFGGGSGPIVLDDVGCSGYETYLMSCSHNPWNTHNCGHSEDASVICSAS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----YDSSD-----LELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAAD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 QIQSTVVPDLMYPTTDYGTESGLALRLVNGSDRCQGRVEVLYRGSWGTVCDDSWDTNDAN 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 VVCRQLGCGWGISAPGDARFGGGSGPIVLDDVGCSGYETYLWSCSHNPWNTHNCGHSEDA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVF 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 LRLVNGDGPCSGTVEVKFQGQWGTVCDDGWNTTASTVVCKQLGCPFSFAM---FRFGQAV 104
                                                                                                                                                                                                                                                                                                                                                                                        -----PDIW-----ESGLALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 LVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 IMLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCS 576
                                                                                                                                                                                                                                                      Similarity 38.5:
                                                                                                                                                                                                                                                                                       Matches 223;
                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                        286 VCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSG 345
                                                                                                                                                                                                                                             346 TVNFDCLHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALV 405
                                                                                                                                                                                                                                                                                                                                                101 DIQET----TETSQTSSPTPDWW-----NHGGTINDVIYD---TQETTEGTDSG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   713 ILCANGWGMNIAEVVCRQLECGSAIRVS----REPHFTERTLHILMSNSGCTGGEASLWD 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIRWEWKQTACHLNMEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSL-- 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       554
                                                                                                                                                                                                                                                                             WLSHNCGHQEDAGVICSD-----SQTSSPTPG-----WW---NPGGTNNDVIY 100
                                                                                                                                                                                              ----GSETHLALCPIV-----QHPEDTC--IHSREVGVVCSRYTDVRLVNGKSQCDGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- PCLANVSDPYLSAVPEG--SALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               647 YNSSLIARV-----CDGSNGSFTSTQ------NFMSVVFITDGSVTRRGFQAD
                                                                                                                                                                                                                                                                                                               106 VCKQLGCPFSVFGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAG
                                                                                                                                                                                                                                                                                                                                                                                  466 VICSDKADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCS-----
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                                                                                                  12.9%; Score 1048.5; DB 2; Length 1290; llarity 29.7%; Pred. No. 4.5e-60; Conservative 114; Mismatches 290; Indels 281;
F;142-245/Domain: scavenger receptor cysteine-rich domain homology F;289-392/Domain: scavenger receptor cysteine-rich domain homology F;833-689/Domain: C1r/C18 repeat homology <C1R1>F;713-816/Domain: scavenger receptor cysteine-rich domain homology F;838-944/Domain: C1r/C18 repeat homology <C1R2>
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Matches 289;
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Cispecies: Strongylocentrotus purpuratus (purple urchin)
Riberence: Zi: Rast, J:P: Davidson, E.H.
Immunogeneitcs 49, 773-786, 1999
A;Title: Origins of immunity: transcription factors and homologs of effector genes (A;Reference number: Z18253; MuID:99328904; PMID:10398804
A;Reference number: Z18253; MuID:99328904; PMID:10398804
A;Reference number: Z18253; MuID:99328904; PMID:10398804
A;Reference: mRNA
A;Reference: mRNA
A;Residues: 1-1036 cPAN>
A;Cross-references: EMBL:AF076513; NID:94164530; PID:94164531; PIDN:AAD05493.1
                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---CKQLGCPFSVFGSRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 DLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLG----CGKPMHVFGMTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 1036;
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 ADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVV-----
                                                                                                                                                                                                                                                                                                                                                                                                   Score 866.5; DB 2
Pred. No. 2.3e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
                                                                                                                                                                                                                                                                                                                                                                                                   10.6%;
llarity 27.1%;
Conservative 8
                   Query Match
Best Local Similarity
Matches 229; Conserv
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Qy         1011 LANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDA 1070           Db         936	Db 546 LCGATLLSSCWVLTAAHCFKRYGNNSRSYAVRVGDYHTLVPEEFEQEIGVQQIVIHRNYR 605  Qy 864 CEGSETHLALCPIVQHPEDTCIH-SREVGVVCSRYTDVRLVNGKSQCDGQVEINVLGHWG 922
RESULT 13 JC5759 Latain-specific serine proteinase (EC 3.4.21) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 31-Mar-2000 C;Accession: JC5759 C;Accession: JC5759 A;Title: Molecular cloning of a novel brain-specific serine crotease with a kringle-like A;Reference number: JC5759; MUID:98008848; PMID:9344839 A;Reference number: JC5759 A;Residues: 1-761 <am> A;Residues: 1-761 <am> A;Residues: 1-761 <am> A;Residues: 1-761 <am 1-761="" 1-771="" <am="" a;residu<="" a;residues:="" td=""><td>RESULT 14  JC4361  Scavenger receptor Cys-rich epidermal growth factor precursor - sea lamprey C; Species: Petromyzon marinus (sea lamprey) C; Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 21-Jul-2000 C; Accession: JC4361 R; Mayer, W.E.; Tichy, H. Gene 164, 267-271, 1995 A; Title: A cDNA clone from the sea lamprey Petromyzon marinus coding for a scavenger A; Reference number: JC4361, MUID: 96069593; PMID: 7590341 A; Accession: JC4361 A; Reference number: JC4361 A; Reference number: JC4361 A; Residues: 1-918 eMAYA C; Comment: This protein is rich in cysteine and plays a role in intercellular contact C; Comment: This protein: growth factor; receptor; transmembrane protein F; 1-34, Domain: signal sequence #status predicted <sigf 1-34,="" <src1="" c;="" cys-teine-rich="" domain="" domain:="" f;="" factor;="" glycoprotein;="" growth="" homology="" keywords:="" protein="" receptor="" receptor;="" scavenger="" transmembrane=""> F; 25-328, Domain: EGF homology <eg2> F; 295-328, Domain: EGF homology <eg3> F; 295-328, Domain: EGF homology</eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg2></sigf></td></am></am></am></am>	RESULT 14  JC4361  Scavenger receptor Cys-rich epidermal growth factor precursor - sea lamprey C; Species: Petromyzon marinus (sea lamprey) C; Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 21-Jul-2000 C; Accession: JC4361 R; Mayer, W.E.; Tichy, H. Gene 164, 267-271, 1995 A; Title: A cDNA clone from the sea lamprey Petromyzon marinus coding for a scavenger A; Reference number: JC4361, MUID: 96069593; PMID: 7590341 A; Accession: JC4361 A; Reference number: JC4361 A; Reference number: JC4361 A; Residues: 1-918 eMAYA C; Comment: This protein is rich in cysteine and plays a role in intercellular contact C; Comment: This protein: growth factor; receptor; transmembrane protein F; 1-34, Domain: signal sequence #status predicted <sigf 1-34,="" <src1="" c;="" cys-teine-rich="" domain="" domain:="" f;="" factor;="" glycoprotein;="" growth="" homology="" keywords:="" protein="" receptor="" receptor;="" scavenger="" transmembrane=""> F; 25-328, Domain: EGF homology <eg2> F; 295-328, Domain: EGF homology <eg3> F; 295-328, Domain: EGF homology</eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg3></eg2></sigf>
Query Match  8.9%; Score 720.5; DB 2; Length 761;  Best Local Similarity 31.8%; Pred. No. 4.8e-39;  Matches 191; Conservative 80; Mismatches 233; Indels 97; Ga  451 DGKAKRTCFRRSDAGVICSDKADLD-LRVGAHSPCYGRLEVKYGGEWGTVCHD	F;356-389/Domain: BGF homology <eg4> F;410-443/Domain: BGF homology <eg5> F;410-443/Domain: BGF homology <eg5> F;467-565/Domain: BGF homology <eg5> F;866-895/Domain: scavenger receptor cysteine-rich domain homology <src2> F;806-895/Domain: transmembrane #status predicted <twm> F;806-918/Domain: intracellular #status predicted <twm> F;40,545,575,585,814/Binding site: carbohydrate (Asn) (covalent) #status predicted Query Match 8.2%; Score 665; DB 2; Length 918; Best Local Similarity 25.7%; Predicted No. 2.4e-35;</twm></twm></src2></eg5></eg5></eg5></eg4>
OY 504 KWSTRNAAVVCROLGCGRPMHYPEMSTEMSCHIMLDDVSCIGNESNIWBCEHSGWGKH 563 11 1-11-11-11-11-11-11-11-11-11-11-11-11	<pre>Matches 256; Conservative 87; Mismatches 336; Indels 318; Gaps 41; Qy 471 KADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGGGKPMHV- 525</pre>
624 LDCPSIIGMGLGNASTGYGK-IWLDDVSCDGDESDLWSCRNSGWGNNDCSHSED  1:	112 FGMGSGPIWMDEVYCSGSESYLSHCLFNGWNSHDCSHGEDASVICSHDA 586 VGGSNRCSGRLEVYFOGRWGTVCDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTG-YGK
	•
Qy         791	Db 238 FCQHGGTCVEYWNYPYYQCYCPSYWWGINCEYYGAHSTDAPESTILPRAE 287  Qy 747 ERTLHILMSNSGCTGGEASLWDCIR-WEWKQTACHLNMEASLICSAHRQPRLV 798  i   :             1   1   1   1   1   1

Qy 799	GADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCRELNCGDAISLSVGDHFGKGNGLTW 858	qq	
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	AEKEQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLVNGKSQCDGQVEINVL	qa	Ψ
Db 357	QXEPMPAMRNLCGILELPYYQCYCPSY	۲۵ . و	10.
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Oy 978 Db 414	NCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAV 1022	qa XX	7 , 7
Oy 1023 Db 460	PEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVA 1082   STATE	da oy	11.
Qy 1083 Db 512	FNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVICSEFTALR 1142 :	oy oy	12
Oy 1143 Db 567	LYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAPLSKTGS 1202 	da .	13
Oy 1203 Db 610	GEMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGGDTECSGRVE 1260	qa ov	13
Qy 1261 Db 654	IWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDA  :	da Qy	3.
Oy 1316 Db 707	S KGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKSLNASSGHLALILSSIF 1368	qa	4
Qy 1369 Db 758	) GLLLIVLFILFLTWGRVQ-KQKHLPLRVSTRRGSLE 1404 	Search Job tir	tim
RESULT 15 149100 mscd6 precursor C; Species: Mus C; Date: 02-7u1- C; Accies: 03-7u1- C; Accies: 04-7u1- C; Accies: 05-7u1- Mol. Immunol. 3 Mol	- mouse musculus (house mouse) 1996 #sequence_revision 02-Jul-1996.#text_change 05-Nov-1999 1000 Bowen, M.; Neubauer, M.; Aruffo, A. 2, 89-92, 1995 g and characterization of murine CD6. g and characterization of murine CD6. minary; translated from GB/EMBL/DDBJ 26 < RES. ces: EMBL:U12434; NID:g761719; PIDN:AAA64867.1; PID:g761720 scavenger receptor cysteine-rich domain homology scavenger receptor cysteine-rich domain homology SRC2> n: scavenger receptor cysteine-rich domain homology SRC3> 7.7%; Score 626.5; DB 2; Length 626; milarity 28.6%; Pred, No. 4.9e-33;		
Qy 900	VRLVNGKSQCDGQVEI		

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08 IWLDD----MRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKSLNASS---- 1357
                                               50 VRVWGHRFHCLGNESLLDNCOMTVLGAPP-----CIHGNTVSVICTGSLTQPLFPC--- 1010
                                                                                                                                             11 ---LANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDL 1067
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                                                                               -----ROSW-----R 265
98 RRRGSLEE---NLFHEMETCLKREDPHGTRTSDD 1428
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completed: May 12, 2003, 06:43:42 le : 48 secs

VRLVNGKSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTIGGKYIGERS 959 006

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         homo sapien
drosophila
                                  rattus norv
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                          taurus
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Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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061982 m
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01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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ANTICEN WC1.1.
SRCR 1.
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SRCR 10.
                                                                                                                                                                    PRT; 1436 AA
                                                                                                                         ALIGNMENTS
                 NOTC_DROME
FBN1_BOVIN
                                 JAG2_RAT
FBN1_PIG
FBN2_MOUSE
CD5_BOVIN
                                                                                      NTC3_MOUSE
JAG2_MOUSE
                                                                     FBN2_HUMAN
                                                                              LRP1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X63723; CAA45255.1; -.
PIR; $19913; S19913.
PIR; A46496; A46496.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00530; SRCR; 11.
PRINTS; PR00528; SPERACTRCPTR.
SMART; SM00202; SR; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSTIE: PS00420; SRCR_1; 4.
PROSTIE: PS50287; SRCR_2; 11.
Antigen; Repeat; Glycoprotein; SIGNAL
                                                                                                                                                                                                              Antigen WC1.1 precursor.
Bos taurus (Bovine).
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NCBI_TaxID=9913;
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Mammalia; Eutheria;
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TISSUE-Blood;
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P30205;
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                                                            ; Search time 21 Seconds
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         GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                           112892 seqs, 41476328 residues
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MSRE_RABIT
CD5_MOUSE
NTC2_MOUSE
ZAN_MOUSE
CD5_HUMAN
NTC2_HUMAN
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CD5L_HUMAN
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CD6_MOUSE
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1110 TSLWQCPSGPWKYSSCSPKEEAYISCEGRRPKSCPTAAAACTDREKLRLRGGDSECSGRVE 1169
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DATVSSFEGTGSGPIMLDEVNCRGEESQVWRCPSWGWRQHNCNHQEDAGVICSGF--VRL
                                                                                        592 AGGDGPCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAELGCGKAVSVLGHMPFRESDGOV
                                                                                                                               WAEKFOCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLV-NGKSQCDGQVEIN
                                                                                                                                                917 VLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGNESLL
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15-JUN-2002 (Rel. 41, Last annotation update)
Neurotrypsin precursor (EC 3.4.21.-) (Motopsin) (Leydin)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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MEDLINE=98201705; PubMed=9540828;
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R Prodom; PD000395; Allinger,

R SMART; SM00130; KR; 1...

BR SMART; SM00120; Tryp_SPF; 1.

BR SMART; SM00020; Tryp_SPF; 1.

BR SMART; SM00020; KRINGLE_1; FALSE_NEG.

BR PROSITE; PS000420; SRCR_1; 3.

BR PROSITE; PS00420; SRCR_2; 4.

BR PROSITE; PS50240; TRYPSIN_DOM; 1.

BR PROSITE; PS50240; TRYPSIN_DOM; 1.

BR PROSITE; PS00134; TRYPSIN_LIS; 1.

BR PROSITE; PS00135; TRYPSIN_LIS; 1.

BR Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.

RW Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.

RW Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.

RW Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.

RM Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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-> V (IN REF. 2).
VY -> AAL (IN REF. 2).
B66EC946DC208DC8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEGUES: D.1.43, The Chymotrypsin. InterPro: IPR001314; Chymotrypsin. InterPro: IPR0010134; Kringle. InterPro: IPR0010124; Ser_protease_Try. InterPro: IPR001190; Srcr_receptor. Pfam; PF00081; kringle; 1. Pfam; PF00899; trypsin; 1. Pfam; PR00722; CHYMOTRYPSIN. PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00725; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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SRCR
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SRCR
                                         MEDLINE-99203523; PubMed-10103056;
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SEQUENCE OF 615-875 FROM N.A.
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Genew; HGNC:9477; PRSS12.
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875 AA;
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MEROPS;
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15-JUV-2002 (Rel. 41, Last annotation update)
Neurotrypsin precursor (EC 3.4.21.-) (Motopsin) (Brain-specific serine protess 3) (BSSP-3).
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                                                                                         239 WGNHDCSHNEDVTLTCYDSSDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADV 298
                                                                                                                                   160 WGYCDCRHG....SVRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASV 206
                                                                                                                                                                              299 VCKQL----GCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLH 353
                                                                                                                                                                                                                                                                                                                                                                                                  322 GLSGIAKAWHQAYFGEGSGPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCTP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   581
                                                                                                                                                                                                          582 GLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         559 KGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC----DYFGKKASGNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 QNDVSVIC--SDGADLE-LRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                              171 KADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLG--CGKPMHVFGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529 TYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTC--SGDA----TW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              611 ----NKESLSSV--------CGLRL------LHRRQKRIIGGKNSLRG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                              Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931 PEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGN---ESLLDNCQ 980
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    Length 875;
Score 822.5; DB 1;
Pred. No. 3.3e-50;
5; Mismatches 307;
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10.1%; 29.6%;
                                                Conservative
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ID CD5L_HUMAN
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                          CARBOHYD
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                        Gschwend T.P., Krueger S.R., Kozlov S.V., Wolfer D.P., Sonderegger P., "Neurotrypsin, a novel multidomain serine protease expressed in the
                                                                                                                                                                            Biochem. Biophys. Res. Commun. 239:386-392(1997).
-!- FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTECLYTIC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH LEARNING AND MEMORY OPERATIONS.
                                                                                                                                                                                                                                 -1- SUBCELLUIAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL CORTEX, HIPPOCAMPUS
                                                                                                                (amamura Y., Yamashiro K., Tsuruoka N., Nakazato H., Tsujimura A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50240; TRYPSIN_DOW; 1.
PROSITE; PS50240; TRYPSIN_BOW; 1.
PROSITE; PS00134; TRYPSIN_BER; 1.
Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.
SIGNAL 1 21 POTENTIAL.
                                                                                                                                           protease with cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REACTIVE BOND (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERINE PROTEASE.
ZYMOGEN ACTIVATION REGION.
                                                                                                                                        "Molecular cloning of a novel brain-specific serine kringle-like structure and three scavenger receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN. -1- SIMILARITY: CONTAINS 3 SRCR DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD, MGI:1100881; Prss12.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
Pfam; PP00051; Kringle; 1.
Pfam; PP00099; Lrypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; FALSE_NEG.
PROSITE; PS50070; KRINGLE_2; 1.
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                                                              Mol. Cell. Neurosci. 9:207-219(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00018; KRINGLE; FALSE_NEG.
PRINTS; PR00258; SPERACTRCPTR.
PLODOm; PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRCR 1.
SRCR 2.
SRCR 3.
TISSUE=Brain;
MEDLINE=97401523; PubMed=9245503;
                                                                                                     MEDLINE=98008848; PubMed=9344839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE; FALS
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EMBL; D89871; BAA23986.1; -.
HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000395; Krin
SMART; SM00130; KR; 1.
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                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.237; -
                                                                                                                                                                                                                                                          AND AMYGDALA.
                                                  system."
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                                                                                                                                                                    motifs.";
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ACT_SITE
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DISULFID
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15-JUN-2002 (Rel. 41, Last annotation update)
CD5 antigen-like precursor (SP-alpha) (CT-2) (IgM-associated peptide).
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                                                                                                                                                                                                                                   451 DGKAKRTCFRRSDAGVI-----CSDKADLD-LRLVGAHSPCYGRLEVKYQGEWGTVCHD 503
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MEDLINE-9719777; PubMed-9045627;
MEDLINE-9719777; PubMed-9045627;
Gebe J.A., Kiener P.A., Ring H.Z., Li X., Francke U., Aruffo A.;
"Molecular cloning, mapping to human chromosome 1 q21-q23, and cell
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                                                                                                                                                                                                                                                                                                                                       RWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKH
                                                                                                                                                                                                                                                                                                                                                                 NCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDCPSSIIGMGLGNAST----GYGK-IWLDDVSCDGDESDLWSCRNSGWGNNDCSHSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RLLGFKYGKQSSVNHFDGSNRPIWLDDVSCSGKEVSFIQCSRRQWGRHDCSHRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RVEVKHADIWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VC-----BSDFSLHAANVLCRELNCGDAISLSVGDH------FGKGNG---LTWAEKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             606 PDRSDYDIALVRL-QGPGEQCARLSTHVLPACLPLWRERPQKTASNC-----HITG-WG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCLGN---ESLLDNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGVICSDASD-----MELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                864 CEGSETHLALCPIVQHPEDTCIH-SREVGVVCSRYTDVRLVNGKSQCDGQVEINVLGHWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                              DB 1; Length 761;
                                                                                                                                                                                Indels
                                                                            DF507B03712164E6 CRC64;
                                                                                                                                                                              80; Mismatches 233;
                                                                                                                                                         Pred. No. 4.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 AA
                                                                                                                            8.8%; Score 719.5;
31.8%; Pred. No. 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                            MW;
  93
521
569
84118 N
                                                                                                                                                                                Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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  93
521
569
761 AA;
                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606
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                                                                    111 VYDCSHDEDAGASCENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLR 170
                                                                                                                         53 WDIKDVAVLCRELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEE-- 110
                                                                                                                                                                      NEDVTLTCYDSSDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCG 306
                                   134 SHNCYHGEDVGVNC-----YGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May play a role in the regulation of the immune
system. Seems to play a role as an inhibitor of apoptosis.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in thymus, liver, spleen and lymph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A., VARIANT ASN-197, AND FUNCTION IN APOPTOSIS.
MEDLINE-99110826; Pubmed-9892623;
Miyazaki T., Hirokami Y., Matsuhashi N., Takatsuka H., Naito M.;
Mincreased susceptibility of thymocytes to apoptosis in mice lacking AIM, a novel murine macrophage-derived soluble factor belonging to
                                                                                                                                                                                                                                                              307 TAL--HFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICS 362
                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CD5 antigen-like precursor (SP-alpha) (CT-2) (Apoptosis inhibitor expressed by macrophages).
CD5L OR APIG OR AIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                      TAAVVCRQLGCPSSFISSGVVNSPAVLR-PIWLDDILCQGNELALWNCRHRGWGNHDCSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS MET-61; ASN-197 AND ARG-205, TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the scavenger receptor cysteine-rich domain superfamily.";
J. Exp. Med. 189:413-422(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20118142; PubMed-10651944; Gebb J.A., Llewellyn M.-B.C., Hoggatt H., Aruffo A.; Molecular cloning, genomic organization and cell-binding characteristics of mouse Spalpha.";
                                                                                                                                                                                                                                                                                                                                                               352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: Glycosylated.-!- SIMILARITY: CONTAINS 3 SRCR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                               JSE STANDARD; P1
035300; 035301; Q91W05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFICITY, AND GLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; ÅF018268; AAB70571.1; -. EMBL; AF018269; AAB70572.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/c; TISSUE-Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunclogy 99:78-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                 CD5L_NOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nodes
                                                                                                                                                                                                                                                                                                                                                CD5L_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 WNTTASTVVCKQLGCPFSFAM---FRFGQAVTRHGKIWLDDVSCYGNESALWECQHREWG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Tissot J.D., Sanchez J.C., Vuadens F., Scherl A., Schifferli J.A., Hochstrasser D.F., Schneider P., Duchosal M.A.;
"IgM are associated to Spalpha (CD5 antigen-like).";
Electrophoresis 23:1203-1206(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LFS-----LILAICTRPGFLASPSG-----VRLVGGLHRCEGRVEVEQKGQWGTVCDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LFSAVVTCILLLNSC----FLISSFNGTDLELRLVNGDGPCSGTVEVKFQGQWGTVCDDG
uding characteristics of Spalpha, a new member of the scavenger eptor cysteine-rich (SRCR) family of proteins."; Biol. Chem. 272:6151-6158(1997).
                                                                                                                                                                                                                                                                                                         "Two-dimensional polyacrylamide gel electrophoresis analysis of cryoglobulins and identification of an IgM-associated peptide."; J. Immunol. Methods 173:63-75(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                     MEDLINE-94308565; PubMed-8034987; Tissot J.D., Schifferli J.A., Hochstrasser D.F., Pasquali C., Spertini F., Clement F., Frutiger S., Paquet N., Hughes G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.8e-41;
40; Mismatches 139; Indels
                                                                                                                                                                                      Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                  Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40A8BE08F9495D83 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 691.5;
                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                       SEQUENCE OF 20-31, AND BINDING TO IGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001190; Srcr_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRCR
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PRINTS; PR00258; SPERACTRCPTR.
SMART; SM00202; SR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38088 MW;
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41.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
 binding characteristics
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239
346
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                                                                  SEQUENCE FROM N.A.
Miyazaki T., Yusa S.;
"Human CT-2 cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 1
138 2
244 3
347 AA;
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                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11981870;
                                                                                                                                                                                                                                                                                            Schneider P.;
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Matches 14
                                                                                                                                                                        Grafham
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Query Match
Best Local Similarity
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CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                              METAL
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                                                                                                                                                                                                                                                                                                                                                                                      541
                                                                                                                                                                                                                                                                                                                                                                                                 424
                                                                                                                                                                                                                                                    253 TCYDSSDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHF- 311
                                                                                                                                                                                                                                                                                     312 AGLPHIQSGSDV-VWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICSD-GADL-- 367
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                             M., Ohsawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUST oxidase homolog 4 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 4) (Lysyl oxidase related protein C).
LOXL4 OR LOXC.
                                                                                                                                                                                                                                                                                                                      ---ELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAKP
                                                                                                                                                                                                                                                                                                                                                      SNEAR-DIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVGAHS
                                                                                                                                                                                                                                                                                                                                                                                      PCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMT--YFKEASGPIWLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                   Score 664.5; DB 1; Length 352; Pred. No. 1.5e-39;
                                                                                                                                                           V -> M.

S -> N.

W -> R.

S -> N (IN REF. 1; AAB70571).

D -> Y (IN REF. 2).

414984AACEF13B23 CRC64;
                                                                                                                                                                                                                                   Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21316447; Pubmed=11292829;
Ito H., Akiyama H., Iguchi H., Iyama Ki K., Miyamoto
                                                                          Apoptosis; Polymorphism.
                                                                                                                          CD5 ANTIGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                 DVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCS 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  757 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                MGD; MGI:1333862; Ap16.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00530; SRCR: 3.
                                                                                                   SRCR
SRCR
SRCR
                                                                                                                                                                                                           8.2%; Scc.
39.1%; Pred
                                                                                                                                                                                   S D
AF011428; AAD01445.1; -. BC006799; AAH06799.1; -.
                                                SMART; SM00202; SR; 3.
PROSITE; PS00420; SRCR_1; 1.
PROSITE; PS50287; SRCR_2; 3.
Signal; Repeat; Glycoprotein;
                                          PRINTS; PR00258; SPERACTRCPTR.
                                                                                                                                                                                                    38835 MW;
                                                                                                                                                                                                                             Best Local Similarity 39.19
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                            61
197 1
205 2
13
113 1
352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090
                                                                                           22
27
141
246
99
195
316
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Q924C6;
                                                                                                                                                                                    CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                            CARBOHYD
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"Molecular cloning and biological activity of a novel lysyl oxidase-
related gene expressed in cartilage.";
J. Biol. Chem. 276:24013-24029(2001).
-:- EUNCTION: May modulate the formation of a collagenous
extracellular matrix.
-:- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).
-:- SMBCELLULAR LOCATION: Extracellular (Potential).
-:- PIM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF
--- PTM: THE LYSING-TROSYLONINNED TO THE EPSILON-AMINO GROUP OF A
LYSINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPPER (POTENTIAL).
CROSS-LINKED TO TYROSYLQUINONE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
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PROSITE; PS00926; LYSYL_OXIDASE; FALSE_NEG.
PROSITE; PS00420; SRCR_1; 1.
PROSITE; PS50287; SRCR_2; 4.
OXIDOREDUCTASE; COPPET; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYSYL OXIDASE HOMOLOG 4.
                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 4 SRCR DOMAINS.
SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.8%; Score 633.5; DB 1;
32.0%; Pred. No. 5.2e-37;
Live 67; Mismatches 190;
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SRCR 2.
SRCR 3.
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InterPro; IPR001190; Srcr_receptor.
Pfam; PF01186; Lysyl_oxidase; 1.
Pfam; PF00530; SRCR; 4.
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or send an email to license@isb-sib.ch).
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262 CQVQVAPGRGKLRPACPGGMHAVVSCVAGPHFRRQKPKPTRKESHAEELKVRLRSGAQVG 321
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10-02175; 09JJ39;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-STANDARD NORTH N
                                                                             MGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSC
                                                                                                                                                     322 EGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREALFGAQLGQGLGPIHLSEVRC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:137004; LOX13.

InterPro; IPR001695; Lysyl_oxidase.
InterPro; IPR001190; Srcr_receptor.
IPRINTS; PR00020; SRCR; J.
IPRINTS; PR000202; SR; Lysyl_oxidase; I.
IPR051TE; PS000205; LYSYL_OXIDASE; I.
IPR051TE; PS000205; LYSYL_OXIDASE; I.
IPR051TE; PS000205; SRCR_I; IRIO; IRI
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LYSINE (BY SIMILARITY).
SIMILARITY: CONTAINS 4 SRCR DOMAINS.
SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441 NESALMDCTYDGKAKRTCFR---RSDAGVICSDKA 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 AAADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLH 353
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PR2151, 096RS1;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
Lysyl oxidase homolog 3 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 EVRLRPAVEWGRRPLP---VTEGLVEVRLPEGWSQVCDKGWSAHNSHVVCGMLGFPGEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLDDVSCYGNESALWECQHREWGSHNCYHGEDVGVNC-----YGEANL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FISSGVVNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHD---CSHNEDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 VNMAFYRMLAQKKQHS-----FGLHSVACVGTEAHLSLCSLEFYRANDTTRCSGGNPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 LTCY------DSSDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 VSCVLGPLYATFTGQKKQQHSKPQGEARVRLKGGAHQGEGRVEVLKAGTWGTVCDRKWDL
                                                                                                                                                                                   CROSS-LINKED TO TYROSYLQUINONE (BY SIMILARITY)
SIMILARITY)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSS--
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              .06
                                                                                                                                                                                                                                                                                                                                                                                                  Length 754;
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                                                                                                                                                                                                                                                                                                                                                           F8758400943F4FF2 CRC64;
  OXIDASE HOMOLOG 3.
                                                                                                                                                                                                                                                                                                                                                                                                7.7%; Score 629; DB 1; L
31.0%; Pred. No. 1.1e-36;
ive 72; Mismatches 183;
                                                                                                      LYSYL-OXIDASE LIKE.
COPPER (POTENTIAL).
COPPER (POTENTIAL).
                                                                                                                                                COPPER (POTENTIAL)
COPPER (POTENTIAL)
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267
391
482
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754 AA;
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Best Local Simi
Matches 155;
                                                                                                                                                                                                                                                      CARBOEYD
CARBOEYD
CARBOEYD
                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
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NCBI_TaxID=9606;
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                                                                                              Matches 167;
CARBOHYD
CARBOHYD
                                    CONFLICT
                                                                        Query Match
                         CARBOHYD
                                                                                    Local
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                                                                                                                                                                                                                                                                             -:- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: EXTRACELLULAR [POTENTIA1).
-:- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES, THE HIGHEST LEVELS.
AMONG THE TISSUES STUDIED BEING SEEN IN THE PLACENTA, HEART, OVARY, TESTIS, SMALL INTESTINE AND SPLEEN.
-:- PTM: THE LYSINE-TYROSYLOJINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
                                                                                                                                                                                                                      K., Xie Y.,
                                                                                                                                               of
                                                                                                                                                                                                                                            'Cloning and characterization of a human lysyl oxidase-like 3 gene
                                                                                                                                                                                                                                                                                                                                                              LYSINE (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
-!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
                                                                                                                                 Jourdan-Le Saux C., Tomshe A., Ujfalusi A., Jia L., Csiszar K.; "Central nervous system, uterus, heart, and leukocyte expression the LOXL3 gene, encoding a novel lysyl oxidase-like protein."; Genomics 74:211-218(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
TYCOSYLOUTNONE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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CROSS-LINKED TO TYROSYLQUINONE (BY
                                   MEDLINE=21181571; PubMed=11284725;
Maki J.M., Kivirikko K.I.;
"Cloning and characterization of a fourth human lysyl oxidase
                                                                                                                                                                                                    MEDLINE-21233589; PubMed-11334717;
Huang Y., Dai J., Tang R., Zhao W., Zhou Z., Wang W., Ying |
Mao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYSYL OXIDASE HOMOLOG 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copper; Glycoprotein; Repeat; Signal
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Genew; HGNC:13869; LOXI3.
InterPro; IPR001169; Lysyl_oxidase.
InterPro; IPR001169; Srcr_receptor.
Fram; PF001186; Lysyl_oxidase; 1.
Fram; PF001186; Lysyl_oxidase; 1.
PRINTS; PR00278; SPERACTRCPTR.
PRODOM; PD013887; Lysyl_oxidase; 1.
SNART; SM00202; SR; 4.
PROSITE; PS00420; LYSYL_OXIDASE; 1.
PROSITE; PS00420; SRCR_1; 1.
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SRCR 2
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SRCR 4
                                                                                                                        MEDLINE-21280915; PubMed-11386757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF282619; AAK51671.1; -.
EMBL; AF311313; AAK63205.1; -.
EMBL; AF284815; AAK91134.1; -.
                                                                                   Biochem. J. 355:381-387(2001).
                                                                                                                                                                                                                                                             (hLOXL3).";
Matrix Biol. 20:153-157(2001)
                                                                                                 [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                            SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 DGWNTTASTVVCKQLGCPFSFA-----MFRFGQAVTRHGKIWLDDVSCYGNESALWECQH 129
                                                                                                                                                                                                                                                                                                                Gaps
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J. Biol. Chem. 276:24023-24029(2001).
                                                                                                                                                                                                                                                                                                                                                                                       30 LLINSCFLISSFNGT-------DLELRLVN-GDGPCSGTVEVKFQGQWGTVCD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 LLL--CLLCSSCLGSPSPSTGPEKKAGSQGLRFRLAGFPRKPYEGRVEIQRAGEWGTICD 71
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LOL4_HUMAN STANDARD;
096DE6; 096EC0: Q96EV1;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 DLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 QGMGAIHLSEVRCSGQELSLWKCPHKNITAEDCSHSQDAGVRCNLPYTGAETRIRLSGGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 VTEGLVEVRLPDGWSQVCDKGWSAHNSHVVCGMLGFPSEKRVNAAFYRLLAQRQCHSFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 HGVACVGTEAHLSLCSLEFYRANDTARCPGGGPAVVSCVPGPVYAASSGQKKQQQSKPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICS---DGADLELRLADGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 RGWGNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEHHLQVEEVRIRPAVGWGRRPLP---
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVVMSGVRCTGTELSLDQCAHHG-THITCKRTGTRFTAGVICSETAS-DLLLHSA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ito H., Akiyama H., Iguchi H., Iyama K., Miyamoto M., Ohsawa K.,
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
E -> K (IN REF. 3).
S82C46DA25E05A69 CRC64;
                                                                                                                                                                                                                                 Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIWINSISCTGNESALWDCTYDGKAKRTCFR---RSDAGVICSDKADLDLRLVGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 DDILCQGNELALWNCRHRGWGNHD---CSHNEDVTLTC----YDSS---
                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                 7.6%; Score 622.5; DB 1;
11.2%; Pred. No. 3.1e-36;
ve 71; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 REWGSHNCYHGEDVGVNC-----YGEANL----
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TISSUE=Testis;
MEDLINE=21316447; PubMed=11292829;
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SEQUENCE FROM N.A.
MEDLINE=21550107; Pubmed=11691589;
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83166 N
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       390
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753 AA;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).
SUBCELLULAR LOCATION: Extracellular (Potential).
TISSUE SPECIFICITY: Expressed in many tissues, the highest levels among the tissues studied being in the skeletal muscle, testis and pancreas. Expressed in cartilage.
PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL EXEIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A LYSINE (BY SIMILARITY).
SIMILARITY: CONTAINS 4 SRCR DOMAINS.
SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
                                                                                                                                                                                                             "A novel human lysyl oxidase-11ke gene (LOXL4) on chromosome 10q24 has an altered SRCR domain and is down-regulated by H-ras.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
Maki J.M., Tikkanen H., Kivirikko K:I.; "Cloning and characterization of a fifth human lysyl oxidase isonergue: the third member of the lysyl oxidase-related subfamily with four scavenger receptor cysteine-rich domains."; Matrix Biol. 20:493-496(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYROSYLQUINONE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CROSS-LINKED TO TYROSYLQUINONE (BY
                                                                                                                                                                      Asuncion L.P., Fogelgren B., Fong K.S.K., Fong S.F.T., Kim Y.,
                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May modulate the formation of a collagenous extracellular matrix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Repeat; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probon; PD013887; Lysyl_oxidase; 1.
Probon; PD013887; Lysyl_oxidase; 1.
PROSITE; PS00420; SRCR_1; 1.
PROSITE; PS50287; SRCR_2; 4.
Oxidoreductase; Copper; Glycoprotein; Repea
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InterPro; IPR001190; Srcr_receptor.
Pfam; PF01186; Lysyl_oxidase; l.
Pfam; PF00530; SRCR; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF338441; AAK71934.1; -.
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                                                                                                                                                                                              Csiszar K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification of a mouse protein homologous to the human CD6 T cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLGCPSSF-ISS------GVVNSPAVLRPIWLDDILCQGNELALWNCR---
                                                                                                                                                 92;
                                                                                                   Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robinson W.H., Prohaska S.S., Santoro J.C., Robinson H.L.,
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                                                                                                                                                 68; Mismatches 191; Indels
542 V -> A (IN REF. 3).
703 Y -> H (IN REF. 3).
84483 MW; 13051ACADB922BBC CRC64;
                                                                                                 Score 618; DB 1;
Pred. No. 6.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=95174761; PubMed=7870060;
Whitney G., Bowen M., Neubauer M., Aruffo A.;
"Cloning and characterization of murine CD6.";
Mol. Immunol. 32:89-92(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD6_MOUSE STANDARD; PRT; 665 AA. 061003; Q61004; Q60679; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) T-cell differentiation antigen CD6 precursor.
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                                                                                                   7.6%; Score 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WDCTYDGKAKRTCFR---RSDAGVICSDKA 472
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MEDLINE=96062291; PubMed=7594475;
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J. Immunol. 155:4739-4748(1995).
                                                                                                                                                    Conservative
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  542 5
703 7
756 AA;
                                                                                                                             Similarity
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                         CONFLICT
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Best Local 8
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                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 960 VRVWGHRFHCLGNESLLDNCQMTVLGAPP-----CIHGNTVSVICTGSLTQPLFPC--- 1010
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NSDSSTSSEEGYCNDPSSKPPPWNSQAFYS -> KDKASGV
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                             3; ARE PRODUCED BY ALTERNATIVE SPLICING.
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        SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; 1 (SHOWN HERE),
3: ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 665;
                                                                                                                                                                                                                                     PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS50287; SRCR_2; 3.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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7.6%; Score 614.5; DB 1,
Pred. No. 9.8e-36;
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A -> T (IN REF. 2)
D -> A (IN REF. 2)
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                                                           SIMILARITY: CONTAINS 3 SRCR DOMAINS.
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N-LINKED
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N-LINKED
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PRIAT, PR00330; SRCKK; 3.
PRINTS; PR00258; SPERACTRCPTR.
SMART; SM00202; SR; 3.
                                                                                                                                                                                                                                                                                                                                  SRCR
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-:- SUBGELLULAR LOCATION: EXTRACEILULAR (POTENTIAL).
-:- TISGUE SPECIFICITY: EXPRESSED IN MANY TISSUES. HICHEST EXPRESSION
IN REPRODUCTIVE TISSUES, PLACENTA, UTERUS AND PROSTATE
-:- PTM: THE LYSINE-TYROSYLQUINOUE IS GENERATED BY THE MODIFICATION OF
A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
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                                                                       1128 KEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCG 1187
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"The LOXI2 gene encodes a new lysyl oxidase-like protein and is expressed at high leavels in reproductive tissues.";
- and thigh leavels in reproductive tissues.";
- J. Biol. Chem. 274:12939-12944(1999).
- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                          320
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192 QDDHVVCKQLKCGWAVKALAGLHFTPGQGPIHRDQVNCSGTEAYLWDCPGRPGDQY-CGH 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOL2_HUMAN STANDARD; PRT; 774 AA.

GOY4KG; QOY5KB; QOBW70;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-yll oxidase homolog 2 precursor (EC 1.4.3.) (Lysyl oxidase-like protein 2) (Lysyl oxidase related protein WS9-14).

LOXL2.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jourdan-Le Saux C., Tronecker H., Bogic L., Bryant-Greenwood G.D.
Boyd C.D., Csiszar K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1308 IWLDD---MRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKSLNASS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYSINE (BY SIMILARITY).
SIMILARITY: CONTAINS 4 SRCR DOMAINS.
SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRRGSLEE ---NLFHEMETCLKREDP 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 QQLSTANQAGINNYHPVPITIAKEAP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Spleen, and Placenta;
MEDLINE-99230328; PubMed=10212285;
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                                                                                                                                                   251 KEDAGVVCSE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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SPAPTLSRPLQLCLSSGGKGPSHHSWGAAT (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CP-----FSVFGSRRAKPSNEARDIWINSISCTGNESALWDC-----TYDGKAKR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 FPGERTYNTKVYKMFASRR-----KQRYWPFSMDCTGTEAHISSCKLGPQVSLDPMKNV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICSD----GADLELRLADG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
L-> Q (IN REF. 3).
M-> L (IN REF. 2).
H-> Q (IN REF. 2).
H-> Q (IN REF. 3).
C-> S (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYROSYLQUINONE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.5%; Score 607.5; DB 1; Lengtu .
27.9%; Pred. No. 3.6e-35;
"" "ismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9DF5D25D4824BCCD CRC64;
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                                                                                                                                                                                 InterPro; IPR001695; Lysyl_oxidase.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00530; SRCR; 4.
Pfam; PF01186; Lysyl_oxidase; 1.
                                                                                                                                                                                                                                          PRINTS; PRO0074; LYSYLOXIDASE.
PRINTS; PR00258; SPERACTRCPTR.
ProDom; PD013887; Lysyl_oxidase; 1.
                                                                                                                                                                                                                                                                                                   PROSITE; PS00926; LYSYL_OXIDASE; 1. PROSITE; PS00420; SRCR_1; 1. PROSITE; PS50287; SRCR_2; 4.
                                                                                                             EMBL; U89942; AAB49697.1; -.
EMBL; BC000594; AAH00594.1; -.
EMBL; AF117949; AAD34343.1; -.
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                        SCRNSGWGNNDCSHSEDV------GVICSD-ASDMEL--RLVGGSSRCAGKVEVN 706
                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GGEASLW-DCIR-WEWKQTACH---LNMEASLICSAHRQPRLVGADMPCSGRVEVKH 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowen M.A., Whitney G.S., Neubauer M., Starling G.C., Palmer D.,
Zhang J., Nowak N.J., Shows T.B., Aruffo A.;
Structure and chromosomal location of the human CD6 gene: detection
of five human CD6 isoforms.";
J. Immunol. 158:1149-1156(1997).
I- FUNCTION: INVOLVED IN CELL ADHESION. BINDS TO CD166.
I- SUBCELLULAR LOCATION: Type I membrane protein.
CD6D AND CD6E; ARE PRODUCED BY ALTERNATIVE SPLICING.
I-SIMILARITY: CONTAINS 3 SRCR DOMAINS.
I-DATABASE: NAME-PROW; NOTE-CD guide CD6 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd6.htm".
                                                                                                                                                                                                                                                                                 VCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSG
                                                                                                                                                                                                                                                                                                                                                                                      613 PKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLNGTKVAEGHKASFCL-EDTECEGDIQKNY
                                                                                   560 WGKHNCVHREDVIVTCSGDATW---GLRLVGGSNRCSGRLEVYFQGR----WGTVCDDGW
                                                                                                                           - ESQGCNHEEDAGVRCNTPAMGLQKKLRLNGGRNPYEGRVEVLVERNGSLVWGMVCGQNW
                                                                                                                                                                      NSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIW------LDDVSCDGDESDLW
                                                                                                                                                                                                              469 GIVEAMVVCRQL-----GLGFASNAFQETWYWHGDVNSNKVVMSGVKCSGTELSLA
                                                                                                                                                                                                                                                                                                                                              707 VQGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMS---NSGCT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aruffo A., Melnick M.B., Linsley P.S., Seed B.; The lymphocyte glycoprotein CD6 contains a repeated domain characteristic of a new family of cell surface and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD6_HUMAN STANDARD; PRT; 668 AA.
P30203; Q9UMF2; Q9Y4LO; Q9Y4K9; Q9Y4K7;
P30703Y [Rel. 25, Created)
16-OCT-2001 [Rel. 40, Last sequence update)
16-OCT-2001 [Rel. 40, Last annotation update)
T-cell differentiation antigen CD6 precursor (T12); (TP120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-----CANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDY 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      813 ADTWRSVC----DSDFSLHAANVLCRELNCG--DAISLSVGDH 849
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Mammalia; Eutheria; Primates;
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        1247 RVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTG 1306
                            Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                            NASSGHLALILSSI-FGLLL--VLFILFLTWCRVQKQKHLPLRVS 1396
                                                                                                                                                               382 TIESSVŢVKIENKESRELMLLIPSIVLGILLLGSLIFIAFIL-LRIKGKYALPVMVN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 477-489.
MEDLINE-89184581; PubMed=2538832;
Dangott L.J., Jordan J.E., Bellet R.A., Garbers D.L.;
"Cloning of the mRNA for the protein that crosslinks to the egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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N-LINKED (GLCNAC. . .) (PC
N-LINKED (GLCNAC. . .) (PC
742533E09576BCB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00420; SRCR_1; 4.
PROSITE; PS00420; SRCR_2; 4.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
SIGNAL 1 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 520; DB 1; L
Pred. No. 3.3e-29;
66; Mismatches 208;
                                                                                                                                                                                                                                                                                                 (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                  532 AA
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InterPro; IPR001190; Srcr_receptor.
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PRINTS; PR00258; SPERACTRCPTR.
SMART; SM00202; SR; 4.
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Best Local Similarity 29.1%
Matches 152; Conservative
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                                                                                                                                                                                                                                                                STANDARD;
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485
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NCBL_TaxID=7668;
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115
459
532 AA;
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01-AUG-1990
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ID SPER_STRPU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1067 LSDAHVVCQKLGCGVAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCR 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCROLGC 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN ISOFORM CD6B, ISOFORM CD6C AND ISOFORM CD6D).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 VRLINGSSSCSGIVEVRLEASWEPACGALWDSRAAEAVCRALGCGGAEAASQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LAPPTPELPPPAAGNTSVAANA--TLAGAP-----ALLCSGAEWR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.3%; Score 592; DB 1; Length 668;
28.7%; Pred. No. 3.7e-34;
Live 59; Mismatches 140; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                              PROSITE; PS00420; SRCR_1; 1.
PROSITE; PS50287; SRCR_2; 3.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD6E).
VFMLPI -> GPGPAP (IN REF. 1).
MISSING (IN REF. 2; AAC51162)
EFB434608012C49E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL). SRCR 1.
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email to license@isb-sib.ch)
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Pfam; PF00530; SRCR; 3.
PRINTS; PR00258; SPERACTRCPTR.
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71828 MW;
                              EMBL; X60992; CAA43306.1; -.
EMBL; U66142; AAC51161.1; -.
EMBL; U66144; AAC51162.1; -.
EMBL; U66145; AAC51164.1; -.
EMBL; U66145; AAC51164.1; -.
                                              . U66142; AAC51161.1;
U66143; AAC51162.1;
U66144; AAC51163.1;
U66145; AAC51164.1;
U66146; AAC51165.1;
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                                                                                                                                    PIR; S26741; S26741.
Genew; HGNC:1691; CD6.
                                                                                                                                                                                                                                       SR; 3
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668 AA;
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   or send an
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EMBL; AF125191; AAD20360.1; -
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                              216
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                                                                                                                                                                                                                                         LVNGDGPCSGTVEVKFQGQWGTVCDDGWNTTASTVVCKQLGCPFSFAMFR---FGQAVTR 106
                                                                                   103
                                                                                                           107 HGKIWLDDVSCYGNESALWECQHREWG-SHNCYHGEDVGVNCY--GEANLGLRLVDGNNS 163
                                                                                                                                    104 -- TFWVYKMNCLGNETRLEDCYHRPYGRPWLCNAQWAAGVECLPKDEPQGSLRMILGDVP 161
                                                                                                                                                                                                                                                                                                      271 GPHEGRVEIWHDDAWGTICDDGWDWADANVVCRQAGYRGAVKASGF----KGEDFGFTWA 326
                                                                                                                                                                                                                                                                                                                                   324 -VWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICSDGADLELRLAD-----G 374
                                                                                                                                                                                                                                                                                                                                                             327 PIHTSFVMCTGVEDRLIDCILRDGWTHSCYHVEDASVVCATDDDDTIEIEPKHTRVRIVG 386
                                                                                                                                                                                                                                                                                                                                                                                          SNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSVFGSRRAKPSNEA----- 428
                                                                                                                                                                                                                                                                                                                                                                                                                      MGQGQGRVEVSLGNGWGRVCDPDWSDHEAKTVCYHAGYK---WGASRAAGSAEVSAPFDL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palecanda A., Paulauskis J., Al-Mutairi E., Imrich A., Qin G., Suzuki H., Kodama T., Tryggvason K., Koziel H., Kobzik L.; Suzuki H., Kodama T., Tryggvason K., Koziel H., Kobzik L.; Fale of the scavenger receptor MARCO in alveolar macrophage binding of unopsonized environmental particles."; J. Exp. Med. 189:1497-1506(1999).

-!- FUNCTION: Bind Gram-positive and Gram-negative bacteria.
-!- SUBCELDUAR LOCATION: Type II membrane protein (Probable).
-!- SIMILARITY: CONTAINS I SRCR DOMAIN.
 ----- LR 49
                          MMLOQYCW-------AACLVI---CIAISSVDDVGAEQNYGREAVEGNIR 44
                                                                     269 NRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGSDV----
                                                                                                                                                                   CSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSSFISSGVVNSPA-----VLRPI
                                                                                                                                                                                           162 NEGTLETFWDGAWGSVCHTDFGTPDGNVACROMG----YSRGVKSIKTDGHFGFSTGPI
                                                                                                                                                                                                                       WLDDILCQGNELALWNCRHRGWGN-----HDC--SHNEDVTLTCYDSSDLELRLVGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Macrophage receptor MARCO (Macrophage receptor with collagenous
MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLLNSCFLISSFNGTDLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RDIWINSISCIGNES-ALWDCTYDGKAKRICFRRSDAGVIC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure).
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1034 KRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGE 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- FUNCTION: Bind Gram-positive and Gram-negative bacteria.
-:- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
-:- TISSUE SPECIFICITY: Expressed in subpopulations of macrophages in the spleen and the medullary cord of lymph nodes.
-:- SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
                                                                                                                                                                                                                    Collagen; Transmembrane; Receptor; Glycoprotein; Signal-anchor.

DOMAIN

CYTOPLASMIC (POTENTIAL).

TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kangas M., Brannstrom A., Elomaa O., Matsuda Y., Eddy R., Shows T.B., Tryggvason K.; "Structure and chromosomal localization of the human and murine genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
116-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Macrophage receptor MARCO (Macrophage receptor with collagenous
                                                                                                                                                                                                                                                                                                                                                              SRCR.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C38F18C46505FB1E CRC64;
                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1094 GSGPIWLDDLNCTGTESHLWQCPSRGWGQHDCRHKEDAGVIC 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSGNIWLDDVNCQGTEDSLWNCKKNNWGSHNCNHNEDAGVEC 482
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                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
Interpro; IPR001097; Collagen.
Interpro; IPR001199; Srcr_receptor.
Pfam; PF001391; SACR; 1
Pfam; PF01391; Collagen; 4.
PRINTS; PR002025; SPERACTRCPTR.
ProDom; PD000007; Collagen; 1.
SMART; SM00202; SR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for the macrophage MARCO receptor.";
Genomics 58:82-89(1999).
                                                                                                                                          SMART; SM00202; SR; 1.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS50287; SRCR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE=99265975; Pubmed=10331948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
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52.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 80:603-609(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
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Q60754;
                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DISULFID
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DISULFID
CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                        EMBL outstation
                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-WACHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL)

N-LINKED (GLCNAC. . ) (POTENTIAL)

B09E7601ECA23637 CRC64;
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                      the Swiss Institute of Bioinformatics
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ROSITE; PS00420; SRCR_1; FALSE_NEG.
ROSITE; PS50287; SRCR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR000087; Collagen.
nterPro; IPR001190; Srcr_receptor.
fam; PF00530; SRCR; 1.
fam; PF01391; Collagen; 5.
RINTS; PR00258; SPERACTRCPTR.
robom; P0000007; Collagen; 1.
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;; AAD51136.1; JOINED
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Matches 51; Conserv
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Search completed: May 12, 2003, 06:37:50 Job time: 28 secs

1034 KRLRLVDGDSRCAGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGE 1093

421 QRVRIMGGTNR--GRAEVYINNEWGTICDDDWDNNDATVFCRMIGYS----RGRALSSYGG 475

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Pred. No. 3.9e-206;
5; Mismatches 415;
             US-09-249-200-7
US-08-893-467A-2
US-08-154-365-2
US-08-154-365-2
US-08-249-200-2
US-08-249-200-2
US-08-249-200-6
US-08-3117-2
US-08-973-117-2
US-08-973-145-2
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US-09-518-046-15
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APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRC
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
BARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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Patent No. 6346606
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36.1%;
                                   ; ORGANISM: Homo sapiens
US-09-341-587-3
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Best Local Similarity
Matches 533; Conserv
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1781.313 Million cell updates/sec
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                                                                                                                              Search time 24 Seconds
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5-09-034-916-17
5-09-034-916-13
5-09-034-916-11
5-09-034-916-16
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-09-276-400-7
-09-448-076-7
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US-09-034-916-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                        protein search, using sw mode]
                                                                                                                            May 12, 2003, 06:36:46
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1 MMLPQNSWHIDFGRCCCHQN.
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length: 2000000000
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Match
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629 629 629

1048.5 718.5 691.5

Score

Result No.

622.5 622.5 622.5 607.5 607.5 482 412 347

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Searched:

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Title: Perfect score: Sequence:

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5.30 5.48 5.48 6.08 6.08 6.68 6.83 7.26 7.26 7.86 7.86 7.86 7.86 7.86 7.86 7.86 7.86 7.90	411 GCPI	GCPFSVFGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSD 470	~ · · · ·	RESULT 2 US-08-47C ; Sequenc ; Patent
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965 946 1023 1006 1083 009 1116 1116 11174 11174 11255 019 11267 11315 009 019 019 019 029 039 039 049 049 059 069 079 079 079 079 079 079 079 07	SAF 11 SAS HFC	DTWRSVCDSDFSLHAANVLCRELNCGDAISLS 84     : DTWPT		T F
GGCGVAF 1083	S-2 1-8	THMDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGH  :		MC US-08-4 US-08-4 Best
	EGSAL     ESSL- NATVS	GCGVAE        GCGWAM FTALRL		Match Qy ()
1196 09 1234 0b 1255 09 1267 0b 1315 09	SAPGN SAPGN YSET-       NSTTT	ATQI 111 116 EVNSGY 117		
1255 QY 1267 Db · 1315 QY 1327 Db	8 - 3	RQLGCGENGVVSLAP 119   :  NDTRQIFTSSYNRMTHFRSD 123		
1315 QY 1327 Db	Ĕ ð	TCEDRIRVRGGDTEC 125 : 1   :RLVNLNSSYGLC 126		
	E SE	COLGCGSALAALRDASFGQGTGTIWLDDMRC 131		

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Match 12.9%; Score 1048.5; DB 1; Length 1290; Local Similarity 29.7%; Pred. No. 1.1e-83; Conservative 114; Mismatches 290; Indels 281; Gaps
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                                                                                                                               AL INFORMATION:
PLICANT: Li, Xiao
PLICANT: Snyder, Solomon H
TLE OF INVENTION: Ebnerin: A Secreted von Ebner's Gland
TLE OF INVENTION: Protein Associated with Taste Buds
HBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER FEDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,350B
FILING DATE:
CURRENT APPLICATION: 4350B
FILING DATE:
COMPUTED TO TO THE PROPERTY OF 
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NDDRESSEE: Banner & Witcoff, Ltd.
TREET: 1001 G Street, N.W.
IITY: Washington
                                     2, Application US/08470350B
5. 5684126
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REGISTRATION NUMBER: 33,568
REFERENCE/FOCKET NUMBER: 01
LECOMMUNICATION INFORMATION:
RELEPHONE: 202-508-9100
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LENGTH: 1290 amino acids
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COPOLOGY: linear
LECULE TYPE: protein
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0-350B-2
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TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR
TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND MONOCLONAL
TITLE OF INVENTION: ANTIBODIES THERETO
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         IWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNES 1320
                                                                                                                                                                                         -----TTAIAGIVC---RQLGCGENGVVSL---APLSKTG 1201
                                                                                                                                                                                                                                                                 SGFM-WVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDRIRVRGGDTECSGRVE 1260
                                                            ----ALRLVNGGDRCRGRVEVLYRGSWGTVCDDSWDTNDANVVCRQLGCGWAMSAPGN 113
                                                                                                                                                                                                                                                                                                                                                              -----SFPSDATL----RLVNLNSSYGLCAGRVE
                                        1089 AHFGEGSGPIWLDDLNCTGTESHLMQCPSRGWGQHDCRHKEDAGVICSEFTALRLYSET-
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                                                                                                                 ------ETESCAGRLEVFY - NGTWGS -----
                                                                                                                                                                                                                                                                                                                                                                                                                 1321 FLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKS 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                          382 TLWQCRNRGWFSHNCNHREDAGVICSGNHLST 413
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90 MIDDLEFIELD ROAD, SUITE 200
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CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/039,956
FILING DATE: 06-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034.916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPENATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09034916
Patent No. 6046314
GENERAL INFORMATION:
APPLICANT: GEBE, JOHN A.
APPLICANT: SIADAR, ANTHONY W.
APPLICANT: ARUFFO, ALEJANDRO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: (650) 325-7812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-09-034-916-2
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CITY: MENLO PARK
STATE: CALIFORNIA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PCLANVSDPYLSAVPEG--SALICLEDKRLRLVDGDSRCAGRVEIYHDGFWGTICD, 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGWDLSDAHVVCQKLGCGVAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQCPSRGWGQ 1122
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                                                                                                                                                                                                                                                               ----HAANVLCRELNCGDAISLSVGDHFGKG------NGLTWAEKFQCE--- 865
                                                                                                                                                                                                                                                                                                                                                                                                                                       689 YYSTPIRTSTTPPTTFPIITGNDSSLV-----LRLVNGTNRCEGRVEILYRGSWVPCAD 742
                                                                                                                                                                                       769 CIRWEWKQTACHLNMEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSL-- 826
                                                                                                                                                                                                                            -----KIFVSSMNRVTVVFTDVQLEGG------CNYDXILVF 505
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315 TVCDDSWDTKDANVVCRQLVCGWALSAPGSAHFGQGSGSIVLDDVACTGHEAYLWSCSHR 374
                                      GWGNNDCSHSEDVGVICSDAS-----DM-----ELRLVGGSSRCAGKVEVNVQGAVG 712
                                                                                                             713 ILCANGWGMNIAEVVCRQLECGSAIRVS----REPHFTERTLHILMSNSGCTGGEASLWD 768
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APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT PILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
SARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.1
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35.8%; Pred. No. 6.7e-55;
ive 63; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                               914 EINVLGHWGSLCDTHWDPEDARVLCR-----
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Patent No. 6346606
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Matches 162; Conservative
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ORGANISM: Homo sapiens
US-09-341-587-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 VNMAFYRMLAQKKQHS-----FGLHSVACVGTEAHLSLCSLEFYRANDTTRCSGGNPAV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---DSSDLELRLVGGTNRCMGRVELKIQGRWGŢVCHHKWNN 293
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                                                                                                                        TAAVVCRQLGCPSSFISSGVVNSPAVLR-PIWLDDILCQGNELALWNCRHRGWGNHDCSH 246
                                                                                                                                                                                                                                   AAKVVCRQLGCGRAVLTQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNH 229
                                                                                                         WNTTASTVVCKQLGCPFSFAM---FRFGQAVTRHGKIWLDDVSCYGNESALWECQHREWG 133
                                                                                                                                                           SHNCYHGEDVGVNC----YGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLN 187
                                                                                                                                                                                                                                                                    NEDVTLTCYDSSDLELRLVGGTNRCMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCG 306
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                                                   21 LFSAVVŢCILLLNSC----FLISSFNGTDLELRLVNGDGPCŚGTVEVKFQGQWGTVCDDG 76
                                                                                                                                                                                                                                                                                                                        TAL--HFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICS 362
                                                                                                                                                                                                                                                                                                                                       288 KSLSPSFRDRKCYGPGVGRIWLDNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICS 345
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                                                                    -----GLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSS--
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Length 346;
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 Score 691.5; DB 3;
Pred. No. 6.1e-53;
; Mismatches 139;
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31.0%; Pred. No. 6.7e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/276,400 CURRENT FILING DATE: 1999-03-25 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09276400
Patent No. 6140056
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
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  Query Match
Best Local Simi
Matches 148;
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                                                                                                    SQDAGVRCNLPYTGVETKIRLSGGRSRYEGRVEVQIGIPGHLRWGLICGDDWGTLEAMVA 459
VNMAFY RMLAQKKQHS - - - - - - FGLHSVACVGTEAHLSLCSLEFYRANDTTRCSGGNPAV
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                                                                    QNDVSVICS---DGADLELRLADGSNNCSGRVEVRI----HEQWWTICDQNWKNEQALVV
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TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXII):
FILE REFERENCE: MNI -0.73CP
CURRENT APPLICATION NUMBER: US/09/448,076
CURRENT FILING DATE: 1999-10.23
EARLIER FILING DATE: 1999-10.23
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 754
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31.0%; Pred. No. 6.7e-47;
ive 72; Mismatches 183
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Patent No. 6300092
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Matches 155; Conservative
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19;

us-09-759-130b-381.rai

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APPLICANT: Khodadoust, Mehran et al.
TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
FILE REFERENCE: MI-073CP
CURRENT APPLICATION NUMBER: US/09/448,076
CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/117,580
EARLIER APPLICATION NUMBER: 09/276,400
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
SAFTLER FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 753
         TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: USES THEREFOR FILE REFERENCE: MNI-O73 CURRENT APPLICATION NUMBER: US/09/276,400 CURRENT FILING DATE: 1999-03-25 SOFFWARE: Patentin Ver. 2.0 SOFFWARE: Patentin Ver. 2.0
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| RGWGNSDCTHDEDAGVICKDQRLPGFSDSNVIEVEHHLQVEEVRIRPAVGWGRRPLP--- 183
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Pred. No. 2.5e-46;
1; Mismatches 202;
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APPLICANT: Khodadoust, Mehran
                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 31.2
Matches 167; Conservative
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US-09-276-400-2
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TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: MNI-073
CURRENT APPLICATION NUMBER: US/09/702,572
CURRENT FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID MOS: 10
SOFTWARE: PATENTIN VOF: 2.0
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31.0%; Pred. No. 6.7e-47;
Live 72; Mismatches 183; Indels
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                                                                                                                                                                            Sequence 8, Application US/09702572
Patent No. 6391602
GENERAL INFORMATION:
                   481
                                           519 FTAGVICSETAS-DLLLHSA 537
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                   SDAGVICSDKADLDLRLVGA
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Matches 155; Conservative
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US-09-276-400-2
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Sequence 2, Application US/09702572

Sequence 2, Application US/09702572

GENERAL INFORMATION:

APPLICANT: Khodadoust, Mehran

TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: USES THEREFOR

FILE REFERENCE: MII-O75.

FILE RE
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                                                                                                                                                                                                                                                                                                                                                                                                  DDFTLQAAHILCRELG--FTEATGWTHSAKYGPGT---GRIWLDNLSCSGTEQSVTECAS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSSFISSGVVNSPAVLR---PIWL 219
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                                                                                                        Query Match 7.6%; Score 622.5; DB 4; Best Local Similarity 31.2%; Pred. No. 2.5e-46; Matches 167; Conservative 71; Mismatches 202;
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; Pred. No. 2.5e-46;
71; Mismatches 202;
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CURRENT APPLICATION NUMBER: US/09/702,572
CURRENT FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/2766,400
PRIOR FILING DATE: 1999-03-25
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Best Local Similarity 31.29
Matches 167; Conservative
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                    ORGANISM: Homo sapiens
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LENGTH: 753
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US-09-448-076-2
TYPE: PRT
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APPLICANT: Khodadoust, mehran
ATILLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: USES THEREFOR
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                                                                                                                                                                          SCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSSFISSGVVNSPAVLR---PIWL
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  DGWNTTASTVVCKQLGCPFSFA-
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US-09-276-400-7
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236 FPGERTYNTKVYKMFASRR-----KQRYWPFSMDCTGTEAHISSCKLGPQVSLDPMKNV 289
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27.9%; Pred. No. 5.6e-45;
Live 86; Mismatches 258;
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APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: MNI-073
CURRENT APPLICATION NUMBER: US/09/702,572
CURRENT FILING DATE: 2000-10-31
PRIOR FILING DATE: 1999-03-25
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Patent No. 6391602
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 27.99
Matches 196; Conservative
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US-09-702-572-7
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EARLIER APPLICATION NUMBER: 60/117,580
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-03-25
EARLIER FILING DATE: 1999-03-25
SOFTWARE: PATENTING DATE: 1999-03-25
SOFTWARE: PATENTING DATE: 1999-03-25
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                                                                                                                                                                                                                                                                                                                                                                                                               613 PKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLNGTKVAEGHKASFCL-EDTECEGDIQKNY 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---FSVFGSRRAKPSNEARDIWINSISCTGNESALWDC-----TYDGKAKR 456
 --SDKADLDL-RLVGAHSPCYGRLEVKYQGEWGT 499
                              TCENGLPAVVSCVPGQVFSPDGPSRFRKAYKPEQPLVRLRGGAYIGEGRVEVLKNGEWGT 349
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                                                                                                                                                                                                                  GIVEAMVVCRQL-----GLGFASNAFQETWYWHGDVNSNKVVMSGVKCSGTELSLA
                                                                                                                             560 WGKHNCVHREDVIVTCSGDATW---GLRLVGGSNRCSGRLEVYFQGR----WGTVCDDGW
                                                                                                                                                                                                                                                                                                                          VQGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMS---NSGCT---
                                                              VCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSC1GNESNIWDCEHSG
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27.9%; Pred. No. 5.6e-45;
Live 86; Mismatches 258;
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Best Local Similarity 27.9%
Matches 196; Conservative
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CORGANISM: Homo sapiens
US-09-448-076-7
 TCFRRSDAGVIC - - - .
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US-09-448-076-7
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28; PROTEIN AND NUCLEIC ACID MOLECULES AND 409 468 9 SCRNSGWGNNDCSHSEDV------GVICSD-ASDMEL--RLVGGSSRCAGKVEVN 706 411 260 LELRLVGGTNR-CMGRVELKIQGRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQ 318 410 -ESQGCNHEEDAGVRCNTPAMGLQKKLRLNGGRNPYEGRVEVLVERNGSLVWGMVCGQNW 613 PKNGRHAMIWHDCHRHYHSMEVFTHYDLLNLNGTKVAEGHKASFCL-EDTECEGDIQKNY SGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICSD----GADLELRLADG 116 KGEGPIWLDNLHCTGNEATLAACTSNGWGVTDCKHTEDVGVVCSDKRIPGFKFDNSLINQ 500 VCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSG 613 NSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIW------LDDVSCDGDESDLW GIVEAMVVCROL-----GLGFASNAFQETWYWHGDVNSNKVVMSGVKCSGTELSLA 707 VOGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMS---NSGCT---761...--GGEASLW-DCIR-WEWKQTACH---LNMEASLICSAHRQPRLVGADMPCSGRVEVKH -----GRVEVRIHEQWWTICDQNWKNEQALVVCKQLG 176 IENLNIOVEDIRIRAILSTYRKRIPVMEGYVEVKEGKTWKOICDKHWTAKNSRVVCGMFG ---SDKADLDL-RLVGAHSPCYGRLEVKYQGEWGT 560 WGKHNCVHREDVIVTCSGDATW---GLRLVGGSNRCSGRLEVYFQGR----WGTVCDDGW Length 774; Indels 813 ADTWRSVC----DSDFSLHAANVLCRELNCG--DAISLSVGDH 849 E-----CANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDY 708

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TELEFAX: (650) 325-7823 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 100 amino acids
                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                    TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                             TOPOLOGY:
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APPLICANT: ARUFFO, ALEJANDRO A.
TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR
TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND MONOCLONAL
TITLE OF INVENTION: ANTIBODIES THERETO
                                                                                                                                                                                                                                                                                                                                                                                                  SCRNSGWGNNDCSHSEDV------GVICSD-ASDMEL--RLVGGSSRCAGKVEVN 706
                                                                                                                                                                                                                                                          613 NSKAAAVVCSQLDCPSSIIGMGLGNASTGYGKIW-----LDDVSCDGDESDLW 660
                                                                                                                                                                                                                                                                                                                                                         469 GIVEAMVVCRQL-----GLGFASNAFQETWYWHGDVNSNKVVMSGVKCSGTELSLA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                 520 HCRHDG-----EDVACPQGGVQYGAGVACSETAPDLVLNAEMVQQTTYLEDRPWFM 570
                         ---KORYWPFSMDCTGTEAHISSCKLGPQVSLDPMKNV 289
                                                                                                       290 TCENGLPAVVSCVPGQVFSPDGPSRFRKAYKPEQPLVRLRGGAYIGEGRVEVLKNGEWGT 349
                                                                                                                                                                                         350 VCDDKWDLVSASVVCRELGFGSAKEAVTGSRLGQGIGPIHLNEIQCTGNEKSIIDCKFNA 409
                                                                                                                                                                                                                                  560 WGKHNCVHREDVIVTCSGDATW -- - GLRLVGGSNRCSGRLEVYFQGR -- - - WGTVCDDGW 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761 ---GGEASLW-DCIR-WEWKQTACH---LNMEASLICSAHRQPRLVGADMPCSGRVEVKH 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              613 PKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLNGTKVAEGHKASFCL-EDTECEGDIQKNY 671
                                                                                                                                                  500 VCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSG 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       707 VQGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMS----NSGCT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   672 E-----CANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDY 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       813 ADTWRSVC----DSDFSLHAANVLCRELNCG--DAISLSVGDH
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90 MIDDLEFIELD ROAD, SUITE 200
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APPLICATION NUMBER: US 60/039,956
FILING DATE: 06-WAR-1997
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 04-MAR-1998
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 6046314
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
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APPLICANT: GEBE, JOHN A.
APPLICANT: SIADAK, ANTHONY W.
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MEDIUM TYPE: Floppy disk
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                                                                     TCFRRSDAGVIC-
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TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR
TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND MONOCLONAL
TITLE OF INVENTION: ANTIBODIES THERETO
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                                                           Length 100;
                                                           Score 462; DB 3; Length 10
Pred. No. 1.9e-33;
9; Mismatches 14; Indels
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                                                                                                                                                                                                                                                           Query Match 5.3%; Score 432; DB 3; I Best Local Similarity 71.0%; Pred. No. 8.7e-31; Matches 71; Conservative 13; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
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APPLICATION NUMBER: US 60/039,956
FILING DATE: 06-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09034916 Patent No. 6046314 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GEBE, JOHN A.
APPLICANT: SIADAK, ANTHONY W.
APPLICANT: ARUFFO, ALEJANDRO A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (650) 325-7812
MOLECULE TYPE: DNA (genomic)
                                                              Query Match 5.7%;
Best Local Similarity 77.0%;
Matches 77; Conservative
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MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
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Search completed: May 12, 2003, 06:44:15 Job time : 31 secs

Sequence 148, Sequence 148, Sequence 148,

Sequence 1 Sequence 1 Sequence 1

148,

Sequence 1 Sequence 1

Sequence 148, Sequence 148, Sequence 148, Sequence 114, Sequence 148,

Sequence 1 Sequence 1 Sequence 1

Sequence 114, Sequence 148, Sequence 148,

Sequence 114, Sequence 148, Sequence 148, Sequence 148,

Sequence 1 Sequence 1 Sequence 1

Run on:

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Sequence 11, Application US/10042431
Sequence 11, Application US/10042431
Sequence 11, Application No. US2002018267541
SERERAL INFORMATION:
APPLICANT: MCARTHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: SHAPE, John D
TITLE OF INVENTION: NOVEL GENEE ENCODING PROTEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-602
CURRENT APPLICATION NUMBER: US/10/42,431
CURRENT PILING DATE: 2001-10-25
PRIOR FILING DATE: 2001-10-25
PRIOR FILING DATE: 2000-05-24
SPRIOR FILING DATE: 2000-05-24
SPRIOR FILING DATE: 2000-05-24
SOFFMANDER: DATE OF THE OFFER OFF
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US-09-147-947-6
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FILE REFERENCE: MP100-5350MNIM
CURRENT APPLICATION WUMBER: US/09/759,130B
CURRENT FILING DATE: 2000-016
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-29
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100.0%; Pred. No. 0;
ive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 381, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL GENES E TITLE OF INVENTION: PROGNOSTIC, TITLE OF INVENTION:
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Fraser, Christopher
Sharp, John D
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Myers, Paul S
Leiby, Kevin R
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Oy 1141 LRLYSETE Db 1141 LRLYSETE OY 1201 GSGFWWV OY 1201 GSGFWWV OY 1261 IWHAGSW OY 1261 IWHAGSW OY 1261 IWHAGSW OY 1321 FLWDCHA OY 1341 TWCRYOK OY 1381 TWCRYOK OY 1381 TWCRYOK OY 1441 SLLGVLP OD 1441 SLLGVLP	RESULT 3 US-10-042-431-13 US-10-042-431-13 Sequence 13, App. PUDLICATION NO. GENERAL INFORMAT APPLICANT: BARA APPLICANT: BARA APPLICANT: BARA APPLICANT: FR. TITLE OF INVENT: TITLE OF INVENT: TITLE OF INVENT: TITLE OF INVENT:	CURRENT APPLICY CURRENT FILING PRIOR APPLICATION OF PRIOR FILING DA PRIOR FILING DA NUMBER OF SEQ 13 SOFTWARE: PALCE SEQ ID NO 13 LENGTH: 1413 TYPE: PRT ORGANISM: HOME ORGANISM: HOME S-10-042-431-13 QUETY MATCH BEST LOCAl SIMI]	Matches 1413; G Qy
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BARNES, Thomas M
FRASER, Christopher C
SIARP, John D
NVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
NVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
PLICATION NUMBER: US/10/042,431
LIGG DATE: 2001-10-25
ILGATION NUMBER: US 09/333,159
ING DATE: 1999-06-14
ING DATE: 2000-05-24
SEQ ID NOS: 79
Patentin Ver. 2.1
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APPLICANT: Goodearl, Andrew
APPLICANT: Gottzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIGGNOSTIC, PREVENTIVE,
TITLE OF INVENTION: USES.
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TITLE OF INVENTION:
FILER REPERENCE: MPIO0-5350NIN
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR PELLING DATE: 2000-01-07
PRIOR PELLING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/559,194
PRIOR FILING DATE: 2000-05-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1009-06-30
PRIOR FILING DATE: 1009-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1009-09-10
PRIOR FILING DATE: 1000-06-30
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97.2%; Score 7913; I
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                Dublication No. US20030077777
                                                                                                                                                                                                                         McCarthy, Sean A
Fraser, Christopher C
Sharp, John D
Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Leiby, Kevin R
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Best Local Similarity
                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: HOMO
US-09-759-130B-383
                                                                                                                US-09-759-130B-383
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                                                                                                                                                                                                                                APPLICANT:
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APPLICANT: MCCARTHY, Sean A
APPLICANT: BARRES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
TITLE OF INVENTION: NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRWGTVCHHKWNNAAADVVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWD 340
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100.0%; Pred. No. 0;
ive 0; Mismatches
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blication No. US20020182675A1
NERAL INFORMATION:
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st Local Similarity 100.
tches 1319; Conservative
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0-042-431-14
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ENGTH: 1319
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                                          GYCKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCA
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                            KPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKHNCVHREDVIVTCSGDAT
                                                                                    WGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNAST
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                                                                                                                                    Sequence 384, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
                                                                                                                                                                                McCarthy, Sean A
Fraser, Christopher
Sharp, John D
                                                                                                                                                                                                                   Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
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                                                                                                               RESULT 6
US-09-759-130B-384
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APPLICANT: APPLICANT:

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THERAPEUTIC, AND OTHER
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                                               IOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
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FILE REFERENCE: MPI00-5350MIM
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2000-09-16
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR PRILICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1990-06-14
PRIOR FILING DATE: 1090-05-24
PRIOR FILING DATE: 1090-06-14
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SOFTWARE: FastSEQ for Windows Version 4.0
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FILING DATE: 2000-07-14
APPLICATION NUMBER: US 09/342,364
FILING DATE: 1999-06-29
APPLICATION NUMBER: US 09/608,452
FILING DATE: 2000-06-30
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PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-39
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
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US-09-759-130B-384
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Pred. No. 9e-239;
5; Mismatches 31
                                                                                                          Conservative 166;
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55.2%;
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PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
                                                                                                 Similarity
                                                           Ношо
                 SOFTWARE: Pater
SEQ ID NO 13
LENGTH: 1151
                                                          ; ORGANISM: HOI
US-09-977-577-13
                                                                                                            608;
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APPLICANT: MOLLER, Holger J.
TITLE OF INVENTION ONSTHE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN FILE REFERENCE: MOSSTRUP-1A
CURRENT APPLICATION NUMBER: US/09/977,577
CURRENT APPLICATION NUMBER: US 60/270,120
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
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Patent No. US20020155995A1
GENERAL INFORMATION:
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APPLICANT: MOLLER, Holger J.

TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USE FILE REFERENCE: MOSTRUP-HAEMOGLOBIN RECEPTOR AND THE USE CURRENT APPLICATION NUMBER: US/09/977,577

CURRENT APPLICATION NUMBER: 2001-10-16
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Pred. No. 7.1e-238;
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US-09-977-577-12
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Patent No. US20020155995A1
GENERAL INFORMATION:
APPLICANT: WOESTRUP, Soren
TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE USES
FILE REFERENCE: MOESTRUP-1A
                                                                                              WDCHAKPWGQSDCGHKEDAGVRCSGQSLK----SLNASSGHLALILSSIFGLLLLVLF 1376
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                                   HGGSWGTVCDDSWDLDDAQVVCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSL 1000
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6.8e-238;
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: US 60/270,120
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTING DATE: 2000-10-16
SOFTWARE: PATENTING DATE: 2000-10-16
SOFTWARE: PATENTING DATE: 2010-16
NUMBER OF SEQ ID NOS: 25
LENGTH: 1116
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Similarity 56.2%; Pred. No. 6.8e
38; Conservative 161; Mismatches
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Best Local S:
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Conservative
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                                                         GENERAL INFORMATION:
APPLICANT: MOESTRUP, SOTEN
APPLICANT: MOLER, HOJGET J.
TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR I
FILE REFERENCE: MOESTRUP=1A
CURRENT APPLICATION NUMBER: US, 60/270, 120
PRIOR APPLICATION NUMBER: US, 60/270, 120
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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                              Sequence 11, Application US/09977577 Patent No. US20020155995A1
                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
RESULT 10
US-09-977-577-11
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Sequence 78, Application US/20020182675A1

GENERAL INFORMATION:

APPLICANT: MCCARTHY, Sean A

APPLICANT: BARNES, Thomas M

APPLICANT: FRASER, Christopher C

APPLICANT: BRARP, John D

TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

CURRENT ELING DATE: 2001-10-25

CURRENT APPLICATION NUMBER: US 09/333,159

PRIOR APPLICATION NUMBER: US 09/333,159

PRIOR FILING DATE: 2000-05-24

PRIOR FILING DATE: 2000-05-24

SOFTWARE: PATENTING PATE: 2000-05-24

SOFTWARE: PATENTING PATE: 2000-05-24

SOFTWARE: PATENTING PATE: 2000-05-24

SOFTWARE: PATENTING PATE: 2000-05-24
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                                                                                                                       1001 GPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCPARRWGHSECGHKEDAAVNCTDIS
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DIEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQHMGDCPVTALGASLC
                                          990 IHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRCAGRV
                                                               Length 1436;
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ORGANISM: BOS Sp.
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    Mismatches 495; Indels 154;
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APPLICANT: Wighton, Nicolas
APPLICANT: Wighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman bouglas: A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: NOVEL GENES ENCODING
TITLE OF INVENTION: NOVEL GENES ENCODING
CURRENT FILING DATE: 2000-09-16
PRIOR RELING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR PELING DATE: 2000-06-24
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR PELING DATE: 1999-06-14
PRIOR PELING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR PELING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR PELING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR APPLICATION NUMBER: US 09/602,871
IWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNES 1320
                                                                                      -----QSLKSLNASSGHLALIL 1364
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Pred. No. 7.9e-213;
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NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 448
LENGTH: 1436
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Publication No. US20030022279A1
                                                                                                                                              1321 FLWDCHAKPWGQSDCGHKEDAGVRCSG-
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Fraser, Christopher C
Sharp, John D
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Myers, Paul S
Leiby, Kevin R
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Kirst, Susan J
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Best Local Similarity
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GENERAL INFORMATION:
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Sequence 4, Application US/09147947A
Patent No. US20020160490A1
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Best Local Similarity 31.8
Matches 191; Conservative
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                                                                                                                                                                              EVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVSLAPLSKTGSGFMWVDDIQCPKTH 1216
                                                                                                                                                          1217 ISIWQCLSAPWERRISSPAEETWITCE--------DRIRVRGGDTECSGRVE 1260
                                                                                                                                                                                                                                 IWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNES 1320
                                                                                                                                                                                                                                                                                                                                                                                                      GSLLFLVLVILVTQLLRW-RAER-----RALSSYEDALAEAVYEELDYLLTQKEGLGSP 1342
                                                                                                                                                                                                                                                                                                  FLWDCHAKPWGQSDCGHKEDAGVRCSG-------QSLKSLNASSGHLALIL 1364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09147947A
Patent No. US2020160490A1
GENERAL INFORMATION:
APPLICANT: TSURUCA, No. US20020160490A1uo
APPLICANT: TAMAGUCHI, No. US20020160490A1uo
APPLICANT: TAMAGUCHI, No. US20020160490A1e1
TITLE OF INVENTION: No. US20020160490A1e1
FILE REFERENCE: 001560-349
CURRENT APPLICATION NUMBER: US/09/147,947A
CURRENT FILING DATE: 1997-03-24
EARLIER PILING DATE: 1998-07-24
EARLIER PILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1997-07-24
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Pred. No. 7.7e-51;
96; Mismatches 307;
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29.6%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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Best Local Similarity
Matches 229; Conserv
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471 KADLDLRLVGAHSPCYGRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLG--CGKPMHVFGM 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                822 SDFSLHAANVLCRELNCGDAISLSVGDH-----FGKGNG---LTWAEKFQCEGSETHL 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  872 ALCPIVQHPEDICIH-SREVGVVCSRYTDVRLVNGKSQCDGQVEINVLGHWGSLCDTHWD 930
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                                                                                                                                                      582 GLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDCPSSIIGMGLGNASTG
                                                                                                                                                                                                                                                                        YGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGSSRCAG
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APPLICANT: TARMSHIRO, Kyoko
APPLICANT: TAMAGHIRO, Kyoko
APPLICANT: TAMAGUCHI, No. US20020160490Alomi
APPLICANT: TAMAGUCHI, No. US20020160490Alel
TITLE OF INVENTION: NO. US20020160490Alel Serine Protease
FILE REFERENCE: 001560-349
CURRENT APPLICATION NUMBER: US/09/147,947A
CURRENT PILING DATE: 1997-03-24
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-24
SERIER FILING DATE: 1997-07-24
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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31.8%; Pred. No. 1.8e-43;
ive 80; Mismatches 233;
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                                                                                     677
                                                                                                                                                        367 VGLTCYPDSDGHRLSPGFPIRLVDGENKKEGRVEVFVNGQWGTICDDGWTDKHAAVICRQ 426
                                                                                                                                                                                                                                                                             LECGSAIRVSREPHFTERTLHILMSNSGCTGGEASLWDCIRWEWKQTACHLNMEASLICS 790
                                                                                                                                                                                                                                                                                                             LGYKGPARARTMAYFGEGKGPIHMDNVKCTGNEKALADCVKQDIGRHNCRHSEDAGVICD 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCEHSGWGKH 563
                    NCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQ 623
                                                                                                                                                                                                        VGVICSDASD-----MELRLVGGSSRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQ 730
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                                                                                                                                      LDCPSSIIGMGLGNAST ---- GYGK - IWLDDVSCDGDESDLWSCRNSGWGNNDCSHSED
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Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
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Paoni, Nicholas F.
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Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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Sao, Wei-Qiang
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Eaton, Dan L.
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TAAVVCROLGCPSSFISSGVVNSPAVLR-PIWLDDILCQGNELALWNCRHRGWGNHDCSH 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 SHNCYHGEDVGVNC-----YGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLN 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 I.FSAVVTCILLLNSC----FLISSFNGTDLELRLVNGDGPCSGTVEVKFQGQWGTVCDDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAL--HFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHSGTVNFDCLHQNDVSVICS 362
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Acids Encoding the Same
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Pred. No. 6.7
                                                                                                PRIOR PAILLAND DATE: 2011
PRIOR PLILANG DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PAPLICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR PELICATION NUMBER: PCT/US99/21647
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PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR PAPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
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PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
                                                CURRENT APPLICATION NUMBER: US/09/905,291A CURRENT FILING DATE: 2001-07-12
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Matches 148; Conservative
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Sequence 79, Appl
Sequence 449, App
Sequence 1712, Ap
Sequence 5, Appl1
Sequence 32438, A
Sequence 3, Appl1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MCCARRHY, Sean A
APPLICANT: MCCARRHY, Sean A
APPLICANT: BARRES, Thomas M
APPLICANT: FARSER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERREUTIC, AND OTHER USES
FILE REFERENCE: 10147-602
CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR RILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PATENTIN OF 2.1
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US-09-917-995-32438

US-09-905-2918-147

US-09-907-824-147

US-09-907-824-147

US-09-907-813-147

US-09-906-742-147

US-09-906-742-147

US-09-906-742-147

US-09-907-613-147

US-09-907-613-147

US-09-904-820-147

US-09-904-820-147

US-09-904-820-147

US-09-906-646-147

US-09-906-646-147

US-09-906-646-147

US-09-906-7494-147

US-09-907-7494-147

US-09-907-7494-147

US-09-907-744-113

                              US-09-917-800A-1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/10042431 Publication No. US20020182675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
 Alignment Scores:
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722
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    Command line parameters:
-WODEL-frame+_p2n.model -DEV-x1h
-O=/Cq2_1/USPTO_spool/US09759130/runat_06052003_123555_23406/app_query.fasta_1.1607
-O=/Cq2_2_1/USPTO_spool/US09759130/runat_06052003_123555_23406/app_query.fasta_1.1607
-DB=Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANN=-human40.cd1 -LIST=45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MNN=0 -ALIGN=15 -MODEL-CCAL -OUTFMT-pto -NORM-ext -HEAPSTIZE=500 -MINLEN-0
-MAXLEN=200000000 -USER=US09759130_CCRN_1_1.158_crunat_06052003_12355_23406
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARCAGUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Appl
Sequence 380, App
Sequence 9, Appli
Sequence 379, App
                                                                                                                (without alignments)
7108.859 Million cell updates/sec
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1 MMLPQNSWHIDFGRCCCHQN......CEDASDTSLLGVLPASEATK 1453
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1. /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2. /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
4. /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5. /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6. /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
7. /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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                GenCore version 5.1.4\_p5\_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                     - nucleic search, using frame_plus_p2n model
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US-09-759-130B-380
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US-09-759-130B-379
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext (
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rity: ilarity:	-381 (1-1	etLeuProC             GCTGCCTC	SerAla 	snGlyThrAsi                ATGGAACAGAI	luValLysP)              AGGTGAAATT	erThrvalva 	GlnAlaValT  	eralaLeuT 	spvalGl 	erCysS 	SlyTr 	ellesers 	LeuCysG 	sAspC)	euArgLeuVa            TAAGGCTTG	JTrpGlyT         STGGGGGA	InteuGlyC	spvalvalT
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040	.1 SerCysArgAsnSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAspVaLGlyVal b 	66 198	QY
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0	1 GlyTyrGlyLysIleTrpLeuAspAspVal	64	QY
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20	1) GinGlyArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaValVal 6	09	Qy
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00	1 TrpGlyLeuArgLeuValGlyGlySerAsnArgCysSerGlyArgLeuGluValTyrPh	58	Qy
80	31 GlyLySHisAsnCysValHisArgGluAspValIleValThrCysSerGlyAspAlaThr 5 	56 168	Qy Db
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09	1 AspasspValSerCysIleGlyAsnGluSerAsnIleTrpAspCysGluHisSerGlyTr		δò
40	<pre>11 LysProMetHisValPheClyMetThrTyrPheLysGlualaSerGlyProIleTrpLeu 5-                                      </pre>	52	Qy
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200		144	qq · · ·
00	1. AlaHisSerProCysTyrGlyArgLeuGluValLysTyrGlnGlyGluTrpGlyThrVa	48	QY
80	1 ArgSerAspAlaGlyValIleCysSerAspLysAlaAspLeuAspLeuArgLeuValGly 4	46	Oy do
380	.1 AsnGluSerAlaLeuTrpAspCysThrTyrAspGlyLysAlaLysÀrgThrCysPheArg 4	132	Qy Db
320	CGTGCTAAACCTAGTAATGAAGCTAGA	126	q
40	1 ArgAlaLysProSerAsnGluAlaArgAspIleTrpIleAsnSerIleSerCysThrGl	42	QY
20 260	11 GluGlnAlaLeuValValCysLysGlnLeuGlyCysProPheSerValPheGlySerArg 4	120	Qy Db
200	1 AGAGTAGAGGTGAAATTCATGAACAGTGGTGGACAATATGTGACCAGAACTGGAAGAAT	114	ΩD
00	1 ArgValGluValArgIleHisGluG	38	QY
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90	1 CysArgHisSe	34	QY
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qq	2041	ATCTGTTCTGATGCATGGATATGGAGCTGAGGCTTGTGGGTGG
ος Ο φ	701	GlyLysValGluValAsnValGlnGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGly 720
yo 4	721	rgValSer 740
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Oy Dp	801	rocysSerGlyargValGluValLysHisAlaAspThrTrpArgSerValCys 820 
Oy Dp	821	AspSerAspPheSerLeuHisAlaAlaAlaAsnValLeuCysArgGluLeuAsnCysGlyAsp 840
oy Op	841	AlaIleSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThrTrpalaGlu 860 
Oy Dp	861 2581	<b>□</b> – 0
Qy Dp	881	GluaspThrCysIleHisSerArgGluValGlyValValCysSerArgTyrThraspVal 900 
O. Db	901	ArgLeuvalAsnGlyLysSerGlnCysAspGlyGlnValGluileAsnValLeuGlyHis 920 
Oy Dp	921	TrpGlySerLeuCysAspThrHisTrpAspProGluAspAlaArgValLeuCysArgGln 940 
Qy Db	941	LeuSerCysGlyThrAlaLeuSerThrThrGlyGlyLysTyrIleGlyGluArgSerVal 960 
oy B	961	ArgvaltrpGlyHisArgPheHisCysLeuGlyAsnGluSerLeuLeuAspAsnCysGln 980 
Oy Dp	981 294i	MetthrvalLeuGlyAlaProProCysIleHisGlyAsnThrvalServalIleCysThr 1000 
Qý Db	1001	GlySerLeuThrGlnProLeuPheProCysLeuAlaAsnValSerAspProTyrLeuSer 1020 
Oy Dp	1021 3061	AlavalProGluGlySerAlaLeuIleCysLeuGluAspLysArgLeuArgLeuValAsp 1040
Oy Dp	1041 3121	GlyaspserargCysalaGlyargValGluIleTyrHisaspGlyPheTrpGlyThrIle 1060 

Qy Db	1061 3181	AspLeuSerAspAlaHisValValCysGlnLysL 
Qy Db	1081 3241	PheasnalathrvalSeralaHisPhe 
Qy Db	1101 3301	paspLeuasnCysThrGlyThrGluSerHisLeuTrpGlnCysProSerArgGlyTrp 112 
Qy	1121 3361	ysargHisLysGluaspalaGlyvalIleCysSerGluPheThrala 11 
Oy Db	1141	uTyrSerGluThrGluThrGluSerCysAlaGlyArgLeuGluValPheTyr 116 
Oy Dp	1161	31yThrTrpG1ySerValG1yArgArgAsnIleThrThrAlaIleAlaG1yIleVal 118 
Qy Db	1181	ArgGlnLeuGlyCysGlyGluAsnGlyValValSerLeuAlaProLeuSerLysThr 120 
Qy Db	1201	erGlyPheMetTrpValaspaspIleGlnCysProLysThrHisIleSerIleTrp 122 <sup>i</sup> 
Qy	1221	ysLeuSerAlaProTrpGluArgArgIleSerSerProAlaGluGluThrTrpIle 1 
Oy Db	1241	ysGluaspargIleargValargGlyGlyaspThrGluCysSerGlyargValGlu 12. 
Qy Db	1261 3781	ICysaspaspSerTrpaspLeualaGluala
Qy	1281	/SeralaLeualaalaLeuargaspalaSer 130 
Qy	1301	PheGlyGlnGlyThrGlyThrIleTrpLeuAspAspWetArgCysLysGlyAsnGluSer 1320 
Qy Db	1321	~~~
Qy	1341	erLeuLysSerLeuAsnA                    CGCTGAATCACTGAATG
Qy	1361	×
Qy Db	1381	ysHisLeuProLeuArgValSerThr 
Oy Dp	1401	letGluThrCysLeuLysArgGl 

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240 100 300 120 360 140 420 160 480 180 540 200 009 220 099 240 720 260 780 280 840 300 900

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Conservative:
Mismatches:
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APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Myers, Paul S
APPLICANT: Wrighton, Nicolas
APPLICANT: Wrighton, NogEG
TITLE OF INVEWTION: DAGES.
FILE REFERENCE: WP100-5350MIM
CURRENT APPLICATION NUMBER: US 09/59,130B
CURRENT FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 2000-06-39
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-30
PRIOR PRILCATION NUMBER: US 09/420,707
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                                                                                                                                                                              Sequence 380, Application US/09759130B Publication No. US20030022279A1
                                                                                                                                                                                                                                                    McCarthy, Sean A
Fraser, Christopher
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US-10-042-431-9; Sequence 9, Application US/10042431; Publication No. US20020182675A1

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APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: FRASER, Christopher C
APPLICANT: SHARKS, Thomas M
TITLE OF INVENTION: NOVEL GENES ENCODING PROFIEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-6012
CURRENT APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR PLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PATENTIN VET: 2.1
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ysseraspG1yalaAspLeuG1uLeuArgLeuAlaAspG1; 
luGlnalaLeuValValCysLysGlnLeuGlyCysProPheSerValPh 
AsnGluSerAlaLeuTrpaspCysThrTyraspClyLysAlaLys
LysPrometHisValPheGlymetThrTyrPheLysGluale 
pAspValSerCysIleGlyAsnGluSerAs 
lyLysHisAsnCysValHisArgGluAspValIleValThrCy 

ArgTrpGlyThrValCysAspAspGlyTr 
CCAGCTGCCCATCTTCTATTCATTGCCTTGCCTTGCCTT
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svalGluvalAsnvalGlnGlyàlaval 
rAspPheSerLeuHisAlaAlaAsnVa 
=SerLeuServalGlyAspHisPheGly 
eGInCysGluGlySerGluThrHisLeuAlaLe 
oThrcysileHisSerArgGluValGl. 
JVA1ASnG1yLySSerG1nCySASpG1 
ySerLeuCysAspThrHisTrpAspPr 

	1301 PheGly        3928 TTTGGC	1321 PheLeu         3988 TTTCTA	-		1361 AlaLeu         	1381 ThrTrF         4168 ACGTGG	65 = 62 63 = 63	1421 H1SG1)         4288 CATGG	1441 SerLeu         4348 TCGCTC	RESULT 4 US-09-759-130B-3 ; Sequence 379, ; Publication No	SNEKAL INFORMAPPLICANT: MAPPLICANT: MAPPLI	APPLICANT:	APPLICANT: R APPLICANT: I APPLICANT: V	TITLE OF INVI	CURRENT APPLICATION APPLICATION APPLICATION	PRIOR FILING PRIOR APPLICA PRIOR FILING PRIOR APPLICA	PRIOR FILING PRIOR APPLICA PRIOR FILING PRIOR APPLICA	PRIOR FILLING PRIOR APPLICA PRIOR FILLING PRIOR APPLICA	PRIOR FILING PRIOR APPLICA PRIOR FILING PRIOR APPLICA
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	ThrGlyGlyLysT 	LeuGlyAsnGluS	TTAGGGAATGAGT	IleHisGlyAsnT 	CysLeuAlaAsnV             TGCCTCGCAAATG	CysLeuGluAspL	GlulleTyrH1sA 	AlaHisValValC 	HisPheGlyGluG 	SerHisLeuTrpG                    TCCCACTTGTGGGC	AspalaGlyValI 	GluSerCysAlaG 	ArgasnileThrT                    AGGAACATCACCA	GlyvalvalserL                     GGAGTTGTCAGCC	IleGlnCysProL	ArgileSerSerP 	GlyGlyAspThrG 	ValCysAspAspS 	GlyserAlaLeuA              GCTCTGCTCTGG
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Kirst, Susan J
Mackay, Charles R
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Myers, Paul S
Leiby, Kevin R
Wrighton, Nicolas
Goodearl, Andrew
Holtzman, Douglas A
VENTION: NOVEL GENES ENCODING PROTEINS HAVING
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erLeuGluGluAsnLeuPheHisGluMetGluThrCysLeuLysArgGluAspPro 1420
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LICATION NUMBER: US/09/759,130B
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CATION NUMBER: US 09/479,249
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Fraser, Christopher C
Sharp, John D
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PRIOR APPLICATION NUMBER: US
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NUMBER OF SECTION NOS: 460
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ъ д	641 1948	GlyTyrClyLysIleTrpLeuAspAspValSerCysAspClyAspCluSerAspLeuTrp 660 	
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y a	721	MetasnilealagluvalvalcysargglnLeuglucysglySeralaileargvalSer 740 	•
<u>ې</u>	741	ArgGluProHisPheThrGluArgThrLeuHisIleLeuMetSerAsnSerGlyCysThr 760 	
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qa	3268	CTTCAATGCCACGGTCTCTGCTCACTTTGGGGAGGGGTCAGGGCCCATCTGGGTG
Qy Dp	1101	ISPLeuASNCYSThrGlyThrGluSerHisLeuTrpGlnCysProSerArgGlyTrp 
Qy	1121	InhisaspCysArgHisLysGluAspAlaGlyValIleCysSerGluPheThrAla 
QY	14	rgLeufyrSerGluThrGluThrGluSerCysAlaGlyArgLeuGluValPheTyr
qa ::	3448	AGCTCTACAGTGAAACTGAAACAGAGAGCTGTGCTGGGAGATTGGAAGTCTTCTAT
Qy	1161 3508	[5] [3]
λo d	1181	trgGlnLeuGlyCysGlyGluAsnGlyValValSerLeuAlaProLeuSerLysThr 
o y	20.	ySerGlyphemetTrpValAspAspIleGlnCysProLysThrHisIleSerIleTrp
qq	3628	CTCTGGTTTCATGTGGGTGGATGACATTCAGTGTCCTAAAACGCATATCTCCATATGG
ογ.	2 4	ysLeuSerAlaProTrpGluArgArgIleSerSerProAlaGluGluThrTrpIle
a v	1241	TOCCIOLCIOCCCCATOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
qq	74	- (2
QY	26.	leTrpHisAlaGiySerTrpGlyThrValCysAspAspAspSerTrpAspLeuAlaGluAla   1
qa	3808	CTGGCACGCAGGCTCCTGGGGCACAGTGTGTGATGACTCCTGGGACCTGGCCGAGGCG
Qy	1281	ySerAlaLeuAlaAlaLeuArgAspAlaSer 1
gg ·	ō i	#40101010101000000000000000000000000000
Oy Db	1301	PheGlyGlnGlyThrGlyThrIleTrpLeuAspAspWetArgCysLySGlyAsnGluSer 1320 
. QY	3	PheLeuTrpAspCysHisAlaLysPrOTrpGlyGlnSerAspCysGlyHisLysGluAsp 1
qq	ω Θ	TITCTATGGGACTGTCACGCCAAACCCTGGGGACAGAGTGACTGTGGGGACAAGAGAT.4
Qy Dp	1341	AlaGlyValArgCysSerGlyGlnSerLeuLysSerLeuAsnAlaSerSerGlyHisLeu 1 

262GGCCCCATTTGGCTTTGTATACTTCATGTGAAGGGACAGAGTCAACTGTG 312	125 TrpGluCysGlnHisArgGluTrpGlySerHisAsnCysTyrHisGlyGlu 141 :::   :::	142 AspValGlyValAsnCysTyrGlyGluAlaAsnLeuGlyLeuArgLeuValAspGlyAsn 161	162 AsnSerCysSerGlyArgValGluValLysPheGlnGluArgTrpGlyThrIleCysAsp 181 	182 AspGlyTrpAsnLeuAsnThrAlaAlaValValCysArgGlnLeuGlyCysProSerSer 201 :::                   ::::	202 PheileSerSerGlyValValAsnSerProAlaValLeuArgProIleTrpLeuAspAsp 221	222 IleLeuCysGlnGlyAsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTrpGlyAsn 241	242 HisaspCysSerHisasnGluaspValThrLeuThrCysTyrAspSerSerAspLeuGlu 261	262 LeuargLeuvalGlyGlyThrAsnargCysMetGlyArgValGluLeuLysIleGlnGly 281	282 ArgTrpGlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaAsaValValCysLys 301 :::	302 GlnLeuGlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGlnSerGlySer 321 	322 AspvalValTrpLeuAspGlyValSerCysSerGlyAsnGluSerPheLeuTrpAspCys 341 	342 ArgHisSerGlyThrValAsnPheAspCysLeuHisGlnAsnAspValSerValIleCys 361 :::	362 SerAspGlyAlaAspLeuGluLeuArgLeuAlaAspGlySerAsnAsnCysSerGlyArg 381   11   1026   1018 TCAGGAAAC	382 ValGluValargIleHisGluGlnTrpTrpThrIleCysAspGlnAsnTrpLysAsnGlu 401 :::::::::::	402 GlnAlaLeuValValCysLysGlnLeuGlyCysProPheSerValPheGlySerArgArg 421 	422 AlaLysProSerAsnGluAlaArgAspIleTrpIleAsnSerIleSerCysThrGlyAsn 441 :::::    ::	GluSerAlaLeuTrpAspCysThrTyrAspGlyLysAlaLysArgThrCysPheArgArg 461	1089
qq	Qy Db	Qy Dp	Oy Dp	Qy	Oy Db	Qy	, yo d	Qy Db	Qy Dp	Qy	Qy Db	Qy	Qy Db	Qy Dp	Qy Dp	QY Db	Oy	do Oy
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Qy 1361 AlaLeuIleLeuSerSerIlePheGlyLeuLeuLeuLeuValLeuPheIleLeuPheLeu	1381 ThrTrpCysArgValGlnLysGlnLysHisLeuProLeuArgValSerThrArgArgArgArg		1421 HisGlyThrArgThrSerAspAspThrProAsnHisGlyCysGluAspAlaSerAspThr 	1441 SerleuLeuGlyValLeuProAlaSerGluAlaThrLys 1453 		, Application us/ No. US2002018267 ORMATION: MCCARTHY, Sean A	APPLICANT: BARNES, Thomas M APPLICANT: FRASER, Christopher C APPLICANT: SHARP, John D TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,		PRIOR APPLICATION NUMBER: US 09/333,129 PRIOR FILING DATE: 1999-06-14 PRIOR APPLICATION NUMBER: US 09/578,063 PRIOR FILING DATE: 2000-05-24	NOTER OF SEN 1D NOS: 79 SCOTWARE: Patentin Ver. 2.1 SEO ID NO 79 LENGTH: 4308	) ORGANISM: Bos sp. US-10-042-431-79		37.87% Inches:	OS-09-739-1306-381 (I-1433) X US-10-042-431-79 (I-4308)  Oy 28 CysIleLeuLeuLeuLeuRsnSerCysPheLeuIleSerSerPheAsnGlyThrAspLeuGlu				CCTGGAGG

Tue May

1116 1076 2613 2673 1016 2793 1056 2913 GluValPheTyrAsnGlyThrTrpGlySerValGlyArgArgAsnIleThrThrAlaIle.1176 2253 2313 2373 2493 2553 877 936 2614 TGGAGTTGTCCTGTGACTGCCTTGGGTGGCCTCACTGTTCCCATGGCAACACAGCCTCT ValileCysThrGlySerLeuThrGlnProLeuPheProCysLeuAlaAsnValSerAsp ArgLeuValAspGiyAspSerArgCysAlaGlyArgYalGluIleTyrHisAspGlyPhe TrpG1yThrIleCysAspAspG1yTrpAspLeuSerAspAlaHisValValCysG1nLys GluPheThrAlaLeuArgLeuTyrSerGluThrGluThrGluSerCysAlaGlyArgLeu LeuGlyCysGlyValAlaPheAsnAlaThrValSerAlaHisPheGlyGluGlySerGly ProlleTrpLeuAspAspLeuAsnCysThrGlyThrGluSerHisLeuTrpGlnCysPro TGGGCTGAAGAGTTCAGGTGTGATGGGGGGGGGGCCTGAGCTCTGGTCCTGCCCCAGAGTG CCCTGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGTTCAGTGTAC ||||::||||::|||||::|
ACAGAAGTCCAGCTTATGAAAAACGGCACCTCTCAATGTGAGGGGCAGGTGGAGATGAAG AspAsnCysGlnMetThrValLeuGlyAlaProProCysIleHisGlyAsnThrValSer GTGATCTGCTCAGGAAACCACACCAGGTGCTGCCCCAGTGCAACGACTTCCTGTCTCAA ProTyrLeuSerAlaValProGluGlySerAlaLeuIleCysLeuGluAspLysArgLeu SerArgGlyTrpGlyGlnHisAspCysArgHisLysGluAspAlaGlyValIleCysSer TGTGGCAAGGCTGTGTCTGTCCTGGGACACATGCCATTCAGAGAGTCCGATGGCCAGGTC GlnHisProGluAspThrCysIleHisSerArgGluValGlyValValCysSerArgTyr ThrAspValArgLeuVal---AsnGlyLysSerGlnCysAspGlyGlnValGluIleAsn ValLeuGlyHisTrpGlySerLeuCysAspThrHisTrpAspProGluAspAlaArgVal CysGlyAspAla1leSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThr TrpAlaGluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCysProIleVal GluArgSerValArgValTrpGlyHisArgPheHisCysLeuGlyAsnGluSerLeuLeu 2194 2314 1017 1037 2914 2974 3034 1137 1177 2254 2374 2434 2494 2554 2674 2734 2794 1057 2854 1077 1097 1117 3094 1157 838 828 868 917 937 957 977 997 QQ q Dρ òχ qq g Pp ŏ δ g ò à δλ g δy a δλ õ g a ŏ δy δ ŏ ŏ

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1197 LeuSerLysThrGlySerGlyPheMetTrpValAspAspIleGlnCysProLysThrHis 1216
                                                                                                                                                                                                                                                                                                                                                      TTTGGCCCTGGAAATGGGAGCATCTGGCTGGACGAGGTGCAGTGCGGGGGCCGGGAGTCC 3687
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                                                                   ------AspArgIleArgValArgGlyGlyAspThrGluCysSerGlyArgValGlu
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                         GGTCTCAGGGAAGGTTCTAGACCCCGGTGGGTAGATTTAATTCAGTGTCGGAAAATGGAT
                                                    1217 IleSerIleTrpGlnCysLeuSerAlaProTrpGluArgArgIleSerSerProAlaGlu
                                                                                                                       3925 GCAGAGCGC------AGAGCCTTATCCAGCTATGAAGATGCTTTGCT
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APPLICANT: MCCathly, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 449, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
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Kirst, Susan J
Mackay, Charles R
Myers, Paul S
                                                                                                        GluThrTrpIleThrCysGlu-
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7. 4.	9 (	ValLysPheGlnGluArgTrpGlyThrIleCysAsp 18	
. A	182	alCysArgGlnLeuGlyCysProSerSer 20	
ą	481	GGGAACTTCACACTGCCACTGCCCAGATCATCTGTGCGAGAGTTGGGGTTGTGGCAAGGCT 540	
<u>ک</u> و	202	PhelleSerSerGlyValValAsnSerProAlaValLeuArgProIleTrpLeuAspAsp 221	
λ	222	sn 2	
q	601	99 5	
A	242	HisaspCysSerHisasnGluAspValThrLeuThrCysTyrAspSerSerAspLeuGlu 261	
λ	262	28	
9 2	282	: ;	
, a	7	catgagagcctctgtgcctccactgagctctgccatgccatgttatctgtcg 837	
λ γ	0 6	21	
Q C	ń	AGUITGGCIGIGGAGIIGCCAICICCACCCCGGAGGACCACACIIGGIGGAAGAAGGI 89	
<u>ج</u> ۾	322 898	AspvalvaltrpLeuAspGlyvalSerCysSerGlyAsnGluSerPheLeuTrpAspCys 341	
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ą	1018	01 10	
λ	. 382	ValGluValArgIleHisGluGlnTrpTrpThrIleCysAspGlnAsnTrpLysAsnGlu 401	
q	1027	CAGATCCAGGTGCTTCCCCAG1047	
λ	402	GlnAlaLeuValValCysLysGlnLeuGlyCysProPheSerValPheGlySerArgArg 421	
ð	1048	1GCAACGACTCCGTG 1062	
<u>ک</u> ۾	422	AlaLysProSerAsnGluAlaArgAspileTrpileAsnSerIleSerCysThrGlyAsn 441 :::::   :::         TCTCAACCTACAGGCTCTGCGGCCTCA	
λχ	442	GluSerAlaLeuTrpAspCysThrTyrAspGlyLysAlaLysArgThrCysPheArgArg 461	
ą	1089	1089	
27 28	462	SerAspalaGlyVallleCysSerAspLysAlaAspLeuAspLeuArgLeuValGlyAla 481     ::	
χ̈́	482	TyrGlnGlyGluTrpGlyThrValCy	
ą	1144	GGCGGTCCTGCGCGGGGAGAGTGCTTGACCAGGGCTCCTGGGGCACCATCTGT 1203	
λ	502	<pre>HisAspArgTrpSerThrArgAsnAlaAlaValVySLysGlnLeuGlyCysGlyLys 521  </pre>	

QQ	1204	GATGACGGCTGGGACCTGGACGATGCCCGCGTGTGTGCAGGCAG
οy	522	ProlleTrpLeuAs
qq	1264	
QY	4	61
qq	1324	STGGAGGTGCCCTTCCCGGGGCTGGGG
Qy	562	LysHisAsnCysValHisArgGluAspValIleValThrCysSerGlyAspAlaThrTrp 581 :::
Qy	582	GluValTyrPheGln 60
Dp	1438	ACCAGCAGTGTGCTGGTGGTGGTATTTCTACAAT 14
δλ	602	GlyArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaValValCys 621
QQ	1498	GACCTGGGGCAGTGTCTGCCGTAACCCCATGGAAGACATCACTGTGTCCACGATCTG
Qγ	622	
qq	. 1558	AGCTTGGCTGTGGGGACAGTGGAACCCTCAACTCTTCT
δλ	641	GlyTyrGlyLys1leTrpLeuAspAspValSerCysAspGlyAspGluSer 657
QΩ	1606	
Qy	658	AspLeuTrpSerCysArgAsnSerGlyTrpGlyAsnAspAspCysSerHisSerGluAsp 677
qq	1666	TCTCTCTGGCAGTGTCCTTCTGACCTTGGAATTACAACTCATGCTCTCCAAAGGAGGAA 1725
QY	678	aSerAsp
QQ	1726	GCCTATATCTGGTGTGCAGACAGCAGACAGATCCGCCTGGTGGATGGAGGTGGT 1779
QY	698	ArgCysAlaGlyLysValGluValAsnValGlnGlyAlaValGlyIleLeuCysAlaAsn 717
QQ	1780	CGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGCTCCTGGGGCACCATCTGTGATGAC 1839
δλ	718	GlyTrpGlyMetAsnIleAlaGluValValVySArgGlnLeuGluCysGlySerAlaIle 737
Dp	1840	CGCTGGGACCTGGACGATGCCCGTGTGTGTGTGTGTGTGT
QY	738	ArgValSerArgGluProHisPheThrGluArgThrLeuHisIleLeuMetSerAsnSer 757
QQ	1900	GACGCCACTGTCTTCCTTCGGGACGGGATCAGGGCCCATTGTGGTGAAGTG 1959
Qy	758	GlyCysThrGlyGlyGlualaSerLeuTrpAspCysIleArgTrpGluTrpLysGlnThr 777
qq	1960	AACTGCAGAGAGAGAGTCCCAAAGTATGGAGGTGCCCTTCCTGGGGATGGCGGCAACAC 2019
Qγ	778	eCysSerAlaHisArgGlnProArgLe
qq	2020	AACTGCAATCATCAAGAAGATGCAGGAGTCATGTGCTCAGGATTTGTGCGTCTG 2073
QY	798	lyAlaAspMetProCysSerGlyArgValGluValL
Dp	2074	GCTGGAGGAGATGGACCTGCTCAGGGCGAGTAGAAGTGCATTCTGGAGAAGCTGGACC 2133
QY	818	SerValCysAspSerAspPheSerLeuHisAlaAlaAsnValLeuCysArgGluLeuAsn 837
qq	2134	ATGGAAACTTCACACTCCCCACTGCCCAGGTCATCTGTGCAGAG
δλ	838	CysGlyAspAlaIleSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThr 857
qq	2194	SGCAAGGCTGTGTCTGTGCACACATGCCATTCAGAGAGTCCGATG
Qy	858	TrpAlaGluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCysProIleVal 877
qq	2254	SCTGAAGAGTTCAGGTGTGTGGGGGGGGGGCCTGAGCTCTGGTCCTGCCCCAGAGT

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Š Š	898	ThraspvalargLeuvalAsnGlyLysSerGlnCysAspGlyGlnValGlu1leAsn 916    - - - - - - - - - - - - - - - - - -	
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οy	937	LeuCysargGlnLeuSerCysGlyThrAlaLeuSerThrThrGlyGlyLysTyrIleGly 956	
QQ	2494	:::	
οy	957	GluargSerValArgValTrpGlyHisArgPheHisCysLeuGlyAsnGluSerLeuLeu 976	
g	2554	GAAGGAGGTGATCAGATCTCAACAGCCCAATTTCACTGCTCAGGGGCTGAGTCCTTCCT	
ογ	977	r 996	
Q D	2614	SCCT	
οχ	997	VallleCysThrGlySerLeuThrGlnProLeuPheProCysLeuAlaAsnValSerAsp 1016	
qq	2674	- Fi	
ολ	1017	ProTyrLeuSerAlaValProGluGlySerAlaLeu1leCysLeuGluAspLysArgLeu 1036	
aa	2734	CCTGCAGGCTCTGCGCCTCAGAGAGAGTTCTCCCTACTGCTCAGACAGCAGCAGCTC 2793	
ò	1037	105	
g G	2794	285	
οy	1057	TrpGlyThr11eCysAspAspGlyTrpAspLeuSerAspAlaHisValValCysGlnLys 1076	
Q	2854	TGGGCCACCATCTGTGATGATGACTGGGACCTGGACGCTGTGCTGTGCTGTGCAGGCAG	
ογ	1077	LeuGlyCysGlyValAlaPheAsnAlaThrValSerAlaHisPheGlyGluGlySerGly 1096	
QQ	2914	CTGGGCTGTGGAGAAGCCCTCAATGCCACGGGTCTGCTTCTTCGGGGCAGGATCAGGG 2973	
οy	1097	ProlleTrpLeuAspAspLeuAsnCysThrGluSerHisLeuTrpGlnCysPro 1116	•
q	2974	CCCATCTGGCTGGACGTGCTGAACTGCACAGGAAGGAGTCCCACGTGTGGAGGTGCCCT 3033	
ŏ	1117	SerArgGlyTrpGlyGlnHiSAspCysArgHiSLysGluAspAlaGlyValIleCysSer 1136	
QQ	3034	TCCCGGGGCTGGGGGCGGCACGACTGCAGACACAAGGGGGCCCGGGGCTATTTTTTTT	
οχ	1137	GluPheThralaLeuArgLeuTyrSerGluThrGluThrGluSerCysAlaGlyArgLeu 1156	
qq	3094	GAGTTCCTGGCCCTCAGGATGGTGAGCGAGGACCAGCAGTGTGCTGGTGGCTG 3147	
ò	1157	GluValPheTyrAsnGlyThrTrpGlySerValGlyArgArgAsnIleThrThrAlaIle 1176	
QQ	3148	GAGGTTTTCTACAACGGGACCTGGGGCAGTCTGCCGCAGCCCCCATGGAAGATATCACT 3207	
ογ	1177	AlaGlyIleValCysArgGlnLeuGlyCysGlyGluAsnGlyValValValSerLeuAlaPro 1196	
QQ	3208	GTGTCCGTGATCTGCAGACGATGGATGGAGGACGAGTGCAACACCTCTGTT 3267	
δγ	1197	LeuSerLysThrGlySerGlyPheMetTrpValAspAspIleGlnCysProLysThrHis 1216	
QQ	3268	GGTCTCAGGGAAGGTTCTAGACCCCGGTGGGTATTAATTCAGTGTCGGAAAATGGAT 3327	
ογ	1217	IleSerIleTrpGlnCysLeuSerAlaProTrpGluArgArgIleSerSerProAlaGlu 1236	
qq	3328	ACCTCTCTCTCGCAGTGCTCTTCTGGCCCATGGAAATACAGTTCATGCTCTCTCAAAGGAG 3387	. •

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1321 PheLeuTrpAspCysHisAlaLysProTrpGlyGlnSerAspCysGlyHisLysGluAsp 1340 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                          4027 GATCAGATGACTGGTGCCCTGATGAAATTATGATGATGCTGAAGAAGTACCAGTGCCT 4086
--- 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3808 ACAACCTCAAATTTCTCTCCTGGCATCTTCTCCTGCCTGGGGTTCTCTGCCTTATCCTG 3867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1348 ------GlnSerLeuLysSerLeuAsnAlaSerSerGlyHisLeuAlaLeuIleLeu 1364
                                                                 GAAGCCTACATCTCATGTGAAGGAAGAAGACCCAAGAGCTGTCCAACTGCTGCCGCCTGC
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FILE REFERENCE: 44921-538-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2001-05-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1712, Application US/09917800A Petent No. US20020119462A1 GENERAL INFORMATION:
APPLICANT: Mendrick, Donna APPLICANT: Porter, Mark APPLICANT: Johnson, Kory
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APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
1237 GluThrTrpIleThrCysGlu-
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; PRIOR APPLICATION NUMBER: US 60/290,645 ; PRIOR FILING DATE: 2001-05-15		а ::	496 ACCACA
; PRIOR APPLICATION NUMBER: US 60/292,336 . DRIOR FILING DATE: 2001-05-22		ò	478 LeuVal
FAION FILLING CALL. 2001 02 22 FRIOR APPLICATION NUMBER: US 60/295,798 BIODE FILLING DATE: 2001-06-06		QQ .	
PRIOR PEPLICATION NUMBER: US 60/297,457 PRIOR FILING DATE: 2001-06-13		· o	
PRIOR APPLICATION NUMBER: US 60/298,884  PRIOR FILLING DATE: 2001-06-19		· 6	
PRIOR APPLICATION NUMBER: US 60/303,459 PRIOR FILING DATE: 2001-07-09		δδ	
; NUMBER OF SEQ ID NOS: 1740 ; SOFTWARE: Patentin Ver. 2.1	-	qa	 652 GGCTGT
; SEQ ID NO 1712		٥y	538 IleTrp
; TYPE: DNA ; ORGANISM: Rattus norvegicus		qq	712 ATTGTT
FEATURE: 7. OTHER INFORMATION: Genbank Accession No. US20020119462A1	62A1 NM_022849 ·	ζO	558 SérGly
ZT/T-8008-71/5-60-60-60-60-60-60-60-60-60-60-60-60-60-		q <sub>Q</sub>	772 CGAGGC
Length:	44	Oy.	276
ilarity: 41.73\$ Conservative:		qa.	832 TCTCAA
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		Qy	583
Oy 258 SerAspleuGlübeuArgLeuValGlyGlyThrAsnArgCySMetGlyArgValGlüleu		qq .	952 GATTCT
278		Qy	598 ValTyr
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OY 298 ValValCysLysGinLeuGlyCysGiyThrAlaLouHisPheAlaClyLeuFroHisLeu	siyLeuProHisLeu 31/ 	QQ	1072 AACGTG
7 6		. Qy	638 AlaSer
		qa 	1132 TTTGG
190		Qy	658 AspLeu
338		qa	1192 TATCTG
720		QY	678 Valgly
358 SerVallieCysSerAspGlyAlaAspLeuGluLeuArgLe	, 4	qa	1252 GCTGGA
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3/8 CysSerGiyArgValGiuVaiArgileHisGiuG		qq	1312 ACTACC
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31 97 91	517 651	537	557	576 831	97.6	891	œι	951	597 1011	617	637	131	657 1191	677	, α	ე - რ	4	370	724	418	4.0	.463	760		087
6 ACCACAGAAGGAACAGATTCTGGTTTGGCTGTGAGG 8 LeuvalGlyalaHisSerProCysTyrGlyargLeuGluValLysTyrGlnGlyGluTrp	aAlavalvalCysLysGln 	8 GlycysGlyLysProMetHisValPheGlyMetThrTyrPheLysGluAlaSerGlyPro	### IletrpleuaspaspValSerCyslleGlyAsnGluSerAsnIleTrpAspCysGluHis	8 SerGlyTrpGlyLysHisAsnCysValHisArgGluAspValIleValThrCysSer	9	AGCAGTCCCACACCCGATTCTCAAACAAGCAGTCCCACACACCCGGTTGGT		CCCCGGGGGCACAAATAACGATGTGTCCTATGGACCCGAACAGACCACAGAC	3	8 ValtyrPheGlnGlyArgTrpGlyThrValCysAspAspGlyTrp 	8 AlaValValCysSerGlnLeuAspCysProSerSerIleIleGlyMetGlyLeuGl	2 AACGTGGTGTGCAGGCAGCTGGTCTGTGGCCTGGGCCTTGT	8 AlaserThrGlyTyrGlyLysIleTrpLeuAspAspValSerCysAspGlyAspGluSer	8 AspLeuTrpSerCysArgAsnSerClyTrpClyAsnAsnAsnAspCysSerHisSerGluAsp		8 VAIGLYVALLIECYSSELASPALASEL	9Glu-LeuArgLeuValGlyGlySerSerArgCysAlaGlyLysValG	2 ACTACCACTCCAGAAACTACAACAGATTGGTGGACT-ACAAAATATTCTTCTCTGT	4 uValAsnValGlnGlyAlaValGlyIleLe	1 TACAACACAATTCCCCACCATAGCCGATTGGTGGACAAC	4 aGluValValCysArgGlnLeuGluCysGl	9 GGAATACACCTGTGGAGGTTTACTGACCCT	1 -ArgGluProHisPheThrGluArgThrLeuHisIleLeuM	4 TICCAGCCCATACTACCCTGGAAGCIAICCTAACAATGT	<pre>0 rGlyGlyGluAlaSerLeuTrpAspCysIleArgTrpGluTrpLysGlnThrAlaCysH1       </pre>
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TITLE OF INVENTOR: 0.50 (140.04)   11   11   11   11   11   11   11	19	GACTA		
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SATGPHHISCYSLeuGlyAanGluSerLeuLeuAspAsnCysGlnMetThrValLeuGl 985   SATGPHHISCYSLeuGlyAanGluSerLeuLeuAspAsnCysGlnMetThrValLeuGl 985   SALUER FILING DATE: 1998-07-24	20	CATCCTGGGTTTTGATGGTCCTGAATACAATTCTTCTCTCATTGCTCGGGTT		CURRENT FILING DATE: 1997-03-24; EARLIER APPLICATION NUMBER: PCT/JP98/03324
VOUMBER OF SEQ ID NOS: 6	50 6	<pre>sArgPheHisCysLeuGlyAsnGluSerLeuLeuAspAsnCysGlnMetThrValLeuGl    </pre>		; EARLIER FILING DATE: 1998-07-24 ; EARLIER APPLICATION NUMBER: JP 9/213969 ; EARLIER FILING DATE: 1997-07-24
UTHCOLNE    . 0	yAlaProProCys1leHisGlyAsnThrValSerValIleCysThrGlySerLe		; NUMBER OF SEQ ID NOS: 6 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 5	
UTHINGINPTOLEUPhe	20	AACTTCATGTCTGTAGTCTTTATCACGATGGCAGTGT		; LENGTH: 2562 ; TYPE: DNA
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PG1yPheTrpG1yThr1leCysAspAspG1yTrpAspLeuSerAspAlaHisValValCy 1074	10	SArgLeuArgLeuValAspGlyAspSerArgCysAlaGlyArgValGlulleTyrHisAs		830.00 Matches: 40.26% Conservative: 28.60% Mismatches: 10.20% Indels:
	10	pGlyPheTrpGlyThrIleCysAspAspGlyTrpAspLeuSerAspAlaHisValValCy	:	: -09-759-130B-381 (1-1453) x US-09-147-947-5 (1-2562)

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φy	m	GlyProlleTrpLeuAspAspValSerCysIleGlyAsnGluSerAsnIleTrpAspC
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qq	1236	TCCAGGCGACAGTGGGGGATGACTGCAGCCACCGCGAAGATGTTAGCATTGCCT
δλ	575	yAspAlaThrTrpGlyLeuArgLeuValGlyGl 588
qq	1296	ACCCTGGCGGCGAGGGACACAGGCTCTCTGGGTTTTCCTGTCAGACTGATGGATG
δy	588	ArgTrpGlyThrVa
qq	1356	GAAAATAAGAAAGAAGGACGAGGTGCAGGTTTTTATCAATGGCCAGTGGGGAACAATCT
δy	809	AspaspGlyTrpAsnSerLysAlaAlaAlaValValCysSerGlnLeuAspCysProSe 62
QQ	1416	ALGALGGALGGACTGALAAGGALGCAGCTGTGALCTGTCGTCAGCT
Oy	628	rSerIleIleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyrGlyLysIleTrpLeuAs 648
qq	1476	AAAAGGACCCATCCATGTGG
δλ	648	1yAspGluSerAspLeuTrpSerCysArgAsnSerGlyTrpGl 668
qq	1536	GGAAATGAGAGGTCCTTGGCTGACTGTATCAAGCAAGATATTG
QΛ	899	sSerGluAspValG
QQ	1596	.aactgccgccacagtgaagatgcaggagttatttgr
δy	688	JLeuValGlyGlySerSerArgCysAlaGlyLysValGluValAsnValG
qq	1644	TTTGGCAAGAGGCCTCAGGTAACAGTAA
δy	708	GlyAlaVal
qq	1680	GTCCCTCTCTCTGTT
Qy	728	ysglySerAlaIleArgValSerArgGluProHisPheThrGluA
qq	1696	– v
Qy	748	LeuMetSerAsnSerGlyCysThrGlyGl
q	1722	
Qy	768	pLysGlnThrA
Op	1765	
Qy	788	aHisArgGlnProArgLeuVa
Dp	1795	TCCCATGGAGATGGCAGGCTCTC
Qy	808	rAspPheSerLeuHisAl 82
Dp	1831	CCTGAGTAGCTGCTGGGTCCTCACAGC 18
Qy	828	aAlaAsnValLeuCysArgGluLeuAsnCysGlyAspAlaIleSerLeuSerValGlyAs 848

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AlaalaLeuArgAspAlaSerPheGlyGlnGlyThrGlyThrIleTrpLeuAspAspMet 1313
 LeuAlaProLeuSerLysThrGlySerGlyPheMetTrpValAspAspIleGlnCysPro 1213
                                                            LysThrHisIleSerIleTrpGlnCysLeuSerAlaProTrpGluArgArgIleSerSer 1233
                                                                                                                       ProAlaGluGluThrTrpIleThrCysGluAspArgIleArgValArgGlyGlyAspThr 1253
                                                                                                                                                                                 GluCysSerGlyArgValGluIleTrpHisAlaGlySerTrpGlyThrValCysAspAsp 1273
                                                                                                                                                                                                 30 LeuLeuLeuAsnSerCysPheLeuIleSerSerPheAsnGlyThrAspLeuGluLeuArg 49
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                 162 CCAGCAGAAGAGACCTGGATCACATGTGAAGATAGAATAAGAGTGCGTGGAGGAGAACCC
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APPLICANT: TSURASHIRO, Kyoko
APPLICANT: YAMASHIRO, Kyoko
APPLICANT: YAMAGUCHI, NO. US20020160490Aloni
TITLE OF INVERTION: NO. US20020160490Alel Serine Protease
FILE REFERENCE: 001560-349
CURRENT APPLICATION NUMBER: US/09/147,947A
CURRENT FILING DATE: 1997-03-24
EARLIER APPLICATION NUMBER: PT/JP98/03324
EARLIER FILING DATE: 1998-07-24
NUMBER: OF PT/JP98/03324
EARLIER FILING DATE: 1997-07-24
NUMBER: PAPLICATION NUMBER: JP 9/213969
SEQ ID NOS: 6
SOFTWARE: PALENTIN Ver. 2.0
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.sequence 3, Application US/09147947A
; Sequence 8. Application US/09147947A
; Patent Nc. US20020160490A1
; GENERAL INFORMATION:
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41.54%
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Best Local Similarity:
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CTHER INFORMATION:
US-09-147-947-3
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                                                                                                           1983 TCATCGGGAGTATCGACCGCAGTGATTATGACATAGCCCTGGTTAGATTA---CA 2039
                                                                                                                                                                     2229 ACGTTATAAGGGTCGGTTTACAGGGAGAATGCTTTGTGCTGGAAACCTCCATGAACAAA 2288
                                                            1923 TTATCATACTCTGGTACCAGAGGAGTTTGAGGAAGAAATTGGAGTTCAACAGATTGTGAT 1982
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                                                                                                                                                                                                                                                                                                                                     957
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                                                                                                                                                                                                              897 rThrAspValArgLeuValAsnGlyLysSerGlnCysAspGlyGlnValGluIleAsnVa 917
                                                                                                                                                                                                                                                                         917 lLeuGlyHisTrpGlySerLeuCysAspThrHisTrpAspProGluAspAlaArgValLe 937
                                                                                                                                                   nHisProGluAspThrCysIleHis---SerArgGluValGlyValValCysSerArgTy
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                                                                                        858 pAlaGluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCysProlleValGl
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                              ---PheGlyLysGlyAsnGly-
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Matches:
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LOCATION: (1)...(473)
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ORGANISM: Homo sapiens
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; OTHER INFORMATION: n *
US-09-918-995-32438
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GGACAGCTGCCAGGGAGACAGT------------GGAGACCACTCAT 2391
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---TCATCTGGATGTGGACTGAGGTTACTGCACCGTCG-GCAGAAACGGATCATTGG 1800
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                                              ThrileCysAspGlnAsnTrpLysAsnGluGlnAlaLeuValValCysLysGlnLeu 410
                                                                                                                                             CysproPheSerValPheGlySerArgArgAlaLysProSerAsnGluAlaArgAsp 430
                                                                                                                                                                                                                                                                                                                                                   ----------------SerAlaLeuTrpAspCysThrTyrAspGly--- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                rThrArg-----AsnAlaAlaValValCysLysGlnLeuGlyCysGlyLysProMe 523
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-----GAACAATTCTTTAAGGGTGCCTGGCCTTGGCA----
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1. US20020160374A1
WFORMATION:
T. Genentech, Inc.
T: Ashkenazi, Avi
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GCTC 2544
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Best Local Similarity: 41.34%   Mismatches: 139   Ouery Match: 8.50%   Indels: 31   DB: 9   Gaps: 9   Gaps: 9   Os-09-759-130B-381 (1-1453) x US-09-905-291A-147 (1-1686)   Oy   21 LeuPheSerAlaValValThrCysIleLeuLeuAsnSerCys	LeulleSerSerPheAsnGlyThrAspLeuGluLeuArgLeuValAsnGlyAspGlyPro	Db 194 TGTGAAGGCGGGTGGAGTGGAACAGAAAGGCCAGTGGGCCACCGTGTGTGT	. Oy 97 MetPheargPheGlyGlnAlaValThrArgHisGlyLysIleTrpLeuAsp 113	Oy 114 AspvalSerCysTyrGlyAsnGluSerAlaLeuTrpGluCysGlnHisArgGluTrpGly 133	Qy 134 SerHisAsnCysTyrHisGlyGluAspValGlyValAsnCys147 :::::	168 ValGluValLysPheGlnGluArgTrpGlyThrIleCysAspAspGlyTrpAsnLeuAsn	Db 548 GTGGAAGTGAAGCACCAGAACCAGGGTGGTATACCGTGGCGAGCCTGGGGGCTCGGG 607  Qy 188 ThrAlaalaValValCySArgGlnLeuGlyCySProSerSerPheIleSerSerGlyVal 207	Qy 208 ValAsnSerProalaValLeuArgProileTrpLeuAspAspIleLeuCysGlnGly 226	Qy 227 AsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTrpGlyAsnHisAspCysSerHis 246	Qy 247 AsnGluAspValThrLeuThrCysTyrAspSerSerAspLeuGluLeuArgLeuValGly 266 :::	Qy 267 GlythrAsnArgCysMetGlyArgValGluLeuLysIleGlnGlyArgTrpGlyThrVal 286	Oy 287 CysHisHisLysTrpAsnAsnAlaAlaAlaAspValValCysClysCly 306   1   1   1   1   1   1   1   1   1	Oy 307 ThrAlaLeuHisPheAlaGlyLeuProHisLeuGlnSerGlySerAspValVal 324 :::	Oy 325 TrpLeuAspGlyValSerCysSerGlyAsnGluSerPheLeuTrpAspCysArgHisSer 344
		APPLICANT: Mather J. Jennie P. J. APPLICANT: Pan, James APPLICANT: Pan, James J. APPLICANT: Pan, Margaret Ann J. APPLICANT: Stewart, Times, Daniel J. APPLICANT: APPL	APPLICANT: WOOD, William, I.  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  TITLE OF INVENTION: Acids Encoding the Same  FILE REFERENCE: 10466-14	NT APPLICATION NUMBER: UNT FILING DATE: 2001-07 APPLICATION NUMBER: PCT FILING DATE: 2000-02-22	; PRIOR APPLICATION NUMBER: US 60/143,048 ; PRIOR FILING DATE: 1999-07-07 ; PRIOR APPLICATION NUMBER: US 60/145,698 ; PRIOR FILING DATE: 1999-07-26 ; PRIOR APPLICATION NUMBER: US 60/146,222	; PRIOR FILING DATE: 1999-07-28 ; PRIOR APPLICATION NUMBER: PCT/US99/20594 ; PRIOR FILING DATE: 1999-09 ; PRIOR APPLICATION UMBER: PCT/US99/20944 ; PRIOR FILING DATE: 1999-09-13	PRIOR APPLICATION NUMBER: PCT/US99/21090  PRIOR FILING DATE: 1999-09-15  PRIOR FILING DATE: 1999-09-15  PRIOR APPLICATION NUMBER: PCT/US99/23089	FRIOR FILING DATE: 1999-11-29  PRIOR PAPLICATION NUMBER: PCT/US99/28214  PRIOR FILING DATE: 1999-11-29  PRIOR APPLICATION NUMBER: PCT/US99/28313  PRIOR FILING DATE: 1999-11-30			; PRIOR APPLICATION NUMBER: PCT/US99/30999 ; PRIOR FILING DATE: 1999-12-20 ; PRIOR APPLICATION UMBER: PCT/US00/00219 ; PRIOR FILING DATE: 2000-01-05	; NUMBER OF SEQ ID NOS: 423 ; SEQ ID NO 147 ; LENGTH: 1686 : TYPE: DNA		Arigument Scores: 2.64e-60 Length: 1686 Score: 691.50 Matches: 148 Percent Similarity: 52.51% Conservative: 40

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Alignment Scores:
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TITLE OF INVENTION: Secreted and Transmembra
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CURRENT FILING DATE: 2001-07-10
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FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
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FILING DATE: 1999-09-15
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FILING DATE: 1999-12-16
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ILING DATE: 1999-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/665,350 PRIOR FILING DATE: 2000-09-18
                                                                                                                Sequence 147, Application US/09902853
Publication No. US20020192659A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams, P. Mickey Wood, William, I.
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Stewart, Timothy A.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                          Serritsen, Mary E.
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Mather, Jennie P.
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                                                                                                                                                                                                                            Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                        Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 TrpAsnThrThrAlaSerThrValValCysLysGlnLeuGlyCysProPheSerPheAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 GTTTATGATTGTTCACATGATGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCT
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 147
LENGTH: 1686
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52.518
41.348
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                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-853-147
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Best Local Similarity:
Query Match:
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168 ValGluValLysPheGlnGluArgTrpGlyThrIleCysAspAspGlyTrpAsnLeuAsn 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 TyrGlyGluAlaAsnLeuGlyLeuArgLeuValAspGlyAsnAsnSerCysSerGlyArg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 ThralaAlaValValCysArgGlnLeuGlyCysProSerSerPheIleSerSerGlyVal 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpAsnThrThrAlaSerThrValValCysLysGlnLeuGlyCysProPheSerPheAla
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Matches:
             PRIOR APLICATION NUMBER: PCT/US99/28313
PRIOR PELING DATE: 1999-1130
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLILNG DATE: 1999-12-02
PRIOR PLILNG DATE: 1999-12-02
PRIOR PPLICATION NUMBER: PCT/US99/28565
PRIOR PPLICATION NUMBER: PCT/US99/30095
PRIOR PLICATION NUMBER: PCT/US99/30095
PRIOR PLILNG DATE: 1999-12-16
PRIOR PLILNG DATE: 1999-12-16
PRIOR PLILNG DATE: 1999-12-20
PRIOR PPLICATION NUMBER: PCT/US99/3099
PRIOR PLILNG DATE: 1999-12-20
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FILING DATE: 1999-11-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-147
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Query Match:
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LENGTH: 168
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                     CysHisHisLysTrpAsnAsnAlaAlaAlaAspValValCysLysGlnLeuGlyCysGly 306
                                                                     307 ThrAlaLeu-----HisPheAlaGlyLeuProHisLeuGlnSerGlySerAspValVal 324
                                                                                                                                                                                                                             1082 TTTTGGGGGTTTCACGACTGCACCACCAGGAAGATGTGGCTGTCATCTCCTCA 1135
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APPLICATION NUMBER: PCT/US99/21090
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FILING DATE: 1999-10-05
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FILING DATE: 2000-02-22
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APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: US 60/146,222
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APPLICATION NUMBER: 09/665,350
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Publication No. US20020197671A1
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Grimaldi, Christopher
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ilvaroff, Ellen
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Paoni, Nicholas F.
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Botstein, David
Desnoyers, Luc
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GENERAL INFORMATION
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                                                        227 AsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTrpGlyAsnHisAspCysSerHis 246
                                                                                                                                    CysHisHisLysTrpAsnAsnAlaAlaAlaAspValValCysLysGlnLeuGlyCysGly 306
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728 CGAGAAGCAACCCTTCAGGATTGCCCTTCTGGGCCTTGGGGGAAGAAGAACACCTGCAACCAT 787
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PRIOR FILING DATE: 2000-02-22
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RIOR FILING DATE: 1999-07-07
RIOR APPLICATION NUMBER: US 60/145,698
RIOR FILING DATE: 1999-07-26
RIOR APPLICATION NUMBER: US 60/146,222
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Wood, William, I.
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Stewart, Timothy A.
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 423
SEQ ID NO 147
LENGTH: 1686
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                                      PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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962 AAGTCCCTCTCCCTCCTTCAGAGACCGGAAATGCTATGGCCCTGGGGGTTGGCCGCATC 1021
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668 TGCAACAAGCATGCCTATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGA 727
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                                     227 AsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTrpGlyAsnHisAspCysSerHis
                                                                         728 CGAGAAGCAACCCTTCAGGATTGCCCTTCTGGGCCCTTGGGGGAAGAACACCTGCAACCAT
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FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
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ER: 09/665,350
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Publication No. US20030003530A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Wood, William, I.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 Met------PheArgPheGlyGlnAlaValThrArgHisGlyLysIleTrpLeuAsp 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 LeuIleSerSerPheAsnGlyThrAspLeuGluLeuArgLeuValAsnGlyAspGlyPro 56
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
FILING DATE: 1999-12-02
                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
                                                  APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
                                                                                                                                                                            APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15
US 60/146,222
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ORGANISM: HOMO
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962 AAGTCCCTCTCCTCCTCCTTCAGAGACCGGAAATGCTATGGCCCTGGGGTTGGCCGCATC 1021
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                                                                                                                                                                                                                                                                                                             AsnGluAspValThrLeuThrCysTyrAspSerSerAspLeuGluLeuArgLeuValGly 266
                                                                                                                                                                                                                                                                                                                              GlyThrAsnArgCysMetGlyArgValGluLeuLysIleGlnGlyArgTrpGlyThrVal 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 ThrAlaLeu-----HisPheAlaGlyLeuProHisLeuGlnSerGlySerAspValVal 324
                                                             ValGluValLysPheGlnGluArgTrpGlyThrIleCysAspAspGlyTrpAsnLeuAsn 187
                                                                                                                                                                                     ValAsnSerProAlaValLeuArg---ProIleTrpLeuAspAspIleLeuCysGlnGly 226
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                                                                                               Human TANGO 234 OR
Human TANGO 234 CD
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Human SRCR protein
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"MODEL-frame+_p2n.model - DEV=x1h

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"MODEL-frame+_p2n.model - DEV=x1h

"DB-N_Cencacq_101002 - OFWT-fastap - SUFETX-p2n.rng - MINMATCH-0.1 - LOOPCL-0

- DB-N_Cencacq_101002 - OFWT-fastap - SUFETX-p2n.rng - MINMATCH-0.1 - LOOPCL-0

- LOOPEXT-0 - UNITS-bits - START-1 - SUDD-1 - MARRIX-blosum62 - TRANS-human40.cdi

- LIST-45 - DOCALIGN-200 - THR_SCORE-pct - THR_MAX-100 - THR_MIN-0 - ALIGN-15

- MODE-LOCAL - OUTFWT-pto - NORM-ext - HEAPDIZE-500 - MINLEN-0 - MAXLEN-200000000

- USER-USO9759130_GCGN 1_1_30_gcunat_06052003_123553_23343 - NCPU-6 - ICPU-3

- NO_XRDYX - NO_MMAP - LARGEQUERY - NEG_SCORES-0 - WAIT - LONGLOG - DEV_TIMEOUT=120

- WARN_TIMEOUT-30 - THRRADS-1 - XGAPOP-10 - XGAPORT-0.5 - FGAPOP-6 - FGAPEXT-7
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7336.667 Million cell updates/sec
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The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F44136 and AAF45138-F45139 and AAB66081). The TANGO/INTERCEPT proteins and coding sequences are useful for the TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic autonomic function disorders such as hypertension and sleep disorders, anxiety, and bipolar affective disorder.
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                                                                                                                                              (MILL-) MILLENNIUM PHARM INC.
                                                                               24-MAY-2000; 2000WO-US14858.
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P-PSDB; AAB66037.
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Sequence 4359 BP; 1060 A; 881 C; 1303 G; 1115 T; 0 other;

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CCGGGAAT	yGluAlaAsi            TGAAGCCAA	uVallysP            GGTGAAAT	aAlavalva              TGCCGTGG	nSerProA            TAGCCCTG	uAlaLeuT 	pvalThrL          TGTCACAT	nArgCysM           CCGCTGTA	SLYSTrpA           TAAGTGGA	uHisPheA          TCACTTCG	lsercyss         crccrgcr	eAspCys            TGACTGT	uArgLeuA             GCGACTAG	nTrpTrpT              GTGGTGGA	nLeuGlyC 	gaspiler 	rTyrAspG 	erAspLysA             CTGATAAGG	JGluVal
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ClastyAndPrignTyThVAIDLANGSACALYPABROSECTORANGTOCAGCTGGTG 1860   DB	1741	CTGAGGCTGGTGGCGCGCAGCAACCGCTGCTCGGGAAGACTGGAGGTGTACTTT 18		a è	96
Control   Cont	601	GINGIYArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaAlaAlvalVal 620 		ੂ ਨੂੰ	288
	100	100 - 100 -	-	Qγ	86
Child	1861	%556E.6.IIIIEEUASPC%5FEOSELGELIEELIEGLYMELCLYLEUGLYASUALGSELTIII 04 	•	qq	29
	641	TrofenAspAspValSerCvsAspGlvAspGluSerAspTenTro 66		Qy	100
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ArgGluproHisPheThrGluargThrLeuHisTleLeuMetSerAsnSerGlyCysThr 760	2161			qq	35
	741	Arag]uproHisPhaThrG]uaraThr[anHisT]a[anMatSarAsnSarC]vCvsThr 7	•	Οy	11
61 GlyGlyGluAlaSerLeuTrpAspCys1leArgTrpGluTrpLysGlnThrAlaCysHis 780  61 GlyGlyGluAlaSerLeuTrpAspCys1leArgTrpGluTrpLysGlnThrAlaCysHis 780  62 Fill	2221			QO	33
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ThrTrpG             ACCTGGG
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The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAR45138-F45139 and AAB660857, AAB66085. The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal heard disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheiner's disease, senile dementia, Huntington's disease, amyotrophic autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, bysychoactive substance use disorders, anxiety, and bipolar affective disorder.
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'alG      TGG	uAsnThrAlaAla 	TAA	GInGlyAsnGluLeuAlaLeuTrpAsnC; 	AsnGluAspVa 	GlyThrasnar                 'GGAACTAACCG	Cyshishisly: 	ThralaLeuHis 	AspGlyValSe:                  GATGGTGTCTC	ValAsnPheAs;               GTCAATTTTGA	LeuGluLeuAr             "TTGGAACTGCG	HisGluGlnTr               CATGAACAGTG	CysLysGlnLeuGlyCysP.                        TGTAAGCAGCTAGGATGTC	GluAlaArgAs)                 GAGCTAGAGA	AspCysThrTy                   GACTGCACATA	.IleCysSeras                 ATTTGTTCTGA	yargLe       GAGATT	Thrargasnal	;
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61 Asnasn8 	181 Aspaspo          568 GATGATO	1 SerPhe            TCTTTT	221 Aspilel          688 GACATTT	241 AsnHisP         748 AATCATO	61 GluLeuArgLeu 	81 GlyArgTrpG 	01 LysglnI         28 AAGCAG1	21 SerAsp         88 TCTGAT	1 Cy 3 TG	61 Cysser/         08 TGCTCA(	81 ArgvalGluval 	01 GluGlnAlaLeu 	21 ArgAlal         88 CGTGCT	41 AsnGluSe           48 AATGAGTC	61 ArgSer/         08 AGATCAC	81 Alahis:          68 GCTCATA	01 Cyshis          28 TGTCATC	
Oy 16	Oy 16 Db 56	Oy 20:	Oy 22 Db 68	Qy 24 Db 74	Oy 26	Oy 26 Db 86	Oy 30	Oy 32	Oy 34.	Oy 36 Db 110	Oy 36 Db 116	Oy 4(	Oy 45 Db 128	Qy 44. Db 134	Oy 46 Db 140	Oy 46 Db 146	Oy 5(	ì

ArgGluProHisPheThrGluArgThrLeuHisIleLeuMetSerAsnSerGlyCysThr 760 GluAspThrCysIleHisSerArgGluValGJyValValCysSerArgTyrThrAspVal 900 GlyLysHisAsnCysValHisArgGluAspValIleValThrCysSerGlyAspAlaThr G1yTyrG1yLys11eTrpLeuAspAspVa1SerCysAspG1yAspG1uSerAspLeuTrp IleCysSerAspAlaSerAspMetGluLeuArgLeuValGlyGlySerSerArgCysAla LysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCysProIleValGlnHisPro SerCysArgAsnSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAspValGlyVal AspAspValSerCysIleGlyAsnGluSerAsnIleTrpAspCysGluHisSerGlyTrp 

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Qy Dp	1061 3208	CysaspaspGlyTrpaspLeuSeraspalaHisValValCysGlnLysLeuGlyCysGly 1080 	dy Db	=-0 
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Qy Db	1121 3388	GlyGlnHisAspCysArgHisLysGluAspAlaGlyValIleCysSerGluPheThrAla 1140 	XX XX XX XX XX	3012 JUL
Oy Dp	1141	LeuargLeuTyrSerGluThrGluThrGluSerCysalaGlyArgLeuGluValPheTyr 1160 	DE XX XX XX	r encod
Qy	1161 3508	AsnGlyThrTrpGlySerValGlyArgArgAsnIleThrThrAlatleAlaGlyIleVal 1180 	OS HON XX FH Key FT CDS	Homo sapie Key CDS
Qy Dp	1181 3568	CysargGlnLeuGlyCysGlyGluasnGlyValValSerLeuAlaProLeuSerLysThr 1200 	FF XX PN	WO20011985
Qy Db	1201 3628	GlySerGlyPheMetTrpValAspAspIleGlnCysProLysThrHisIleSerIleTrp 1220 	XX XX YF	22-MAR-200 13-SEP-200
Qy Dp	1221 3688	GincysLeuSerAlaProTrpGluArgArgIleSerSerProAlaGluGluThrTrpIle 1240 	XX PR PR	13-SEP-199 16-SEP-199 20-SEP-199
Oy Dp	1241	ThrcysGluaspargileargvalargGlyGlyAspThrGluCySSerGlyArgValGlu 1260 	PR XX PA	O O E

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Location/Qualifiers
113.3475
/*tage // Argorn // Argorn // Product - "Human secreted protein POLY8"
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The sequence represents the coding sequence of human secreted protein, POLY8. POLYX nucleic acids, polypeptides and antibodies to POLYX can be used for treating or preventing a POLYX associated disorder in a subject, preferably a human. These can be used in the manufacture of a medicament for treating a syndrome associated with a human disease selected from a POLYX associated disorder, where the therapeutic is a POLYX polypeptide, a POLYX nucleotide or a POLXX antibody. They may also be used to screen for a modulator of activity, or latency, or predisposition to a POLXX associated disorder, e.g. cancer.
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                                                                               Claim 9; Page 25-29; 152pp; English.
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                                                     New POLYX polypeptide useful for associated disorder, e.g. cancer
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Db 2762 ATCTCCATATGGCAGTG	dy 1237 GluThrTrpIleThrCy.  D 2822 GAGACCTGGATCACATG	1257	Qy 1277 LeuAlaGluAlaGluVa 	3002	3062	3122	1357 3182	3242	3302	3362	Oy 1437 AlaSerAspThrSerLe Db 3422 GCTAGCGACACATCGCT	344 344			KW cancer; lympnoma; neur KW nervous system disorde KW angiogeneals; stem cel KW genetic disorder; bone		AA OS Homo sapiens. XX XX WO200164834:A2.	XX 07-SEP-2001.
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s monkey; baker's yeast; fission yeast; Norway rat; er; African clawed frog; fruit fly; dog; leukaemia; uroblastoma; autoimmune disorder; cell proliferation; der; inflammatory disorder; cell differentiation; del growth factor; activin; inhibin; cartilage; burn; ne regeneration; tendon; ligament; tissue repair; matic; antiarthitic; vulnerary; antiinflammatory; aouppressive; vasotropic; antiparkinsonian; antidiabetic; antiasthmatic; antiallergic;
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Sequences AAS44576-AAS44919 represent full-length polynucleotides and contig polynucleotides encoding polypeptides of the invention. The DNA and protein sequences are useful for the treatment, diagnosis and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as human, dog, monkey, mouse, hamster or rat. The disorders and a neuroblastoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis, disorders such as Parkinson's disease, Alzhelmer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Mernicke disease, inflammatory disorders such as nephritis, Crohn's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Hernicke disease, inflammatory disorders such as nephritis, Crohn's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Hernicke disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, cell proliferation, cell differentiation, stem cell growth factor, cell proliferation, rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                  Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Tang Z, Wehrman T,
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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use
                                                                                                                                                                                                                                                                                                                                                                  horse;
Ile-----LeuPheLeuThrTrpCysArgValGlnLysGlnLysHisLeuProLeuArg
                                3282 GICGCATTATICTICTIGACTAAAAGCGAAGACAGAGACAGCGG------CTIGCA
                                                                                 ValSerThrArgArgArgGlySerLeuGluGluAsnLeuPheHisGluMetGluThrCys
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                                                                                                                                                                                                                                                                                                                                                                    Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque;
tomatc, monkey; dog; sea urchin; expressed sequence tag; BS
diagnostics; forensic test; gene mapping; genetic disorder;
biodiversity; gene therapy; nutrition; ss.
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J, Werhman T;
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A, Zhang
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3393 CTGAATGCAGATGAT 3407
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Drmanac RA,
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1083 PheAsnAlaThrValSerAlaHisPheGlyGluGlySerGlyProIleTrpLeuAspAsp 1102
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                       2442 ATGAAATGGAAAGGAAAGAATCCCGCATTTGGCAGTGCCATTCACACGGCTGGGGGCAG
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                                                                               LeuAsnCysThrGlyThrGluSerHisLeuTrpGlnCysProSerArgGlyTrpGlyGln
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating disorders
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Zhang J;
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Mismatches:
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Xu C, Xue AJ,
R, Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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20000S-0662191.
20000S-0693036.
Human polynucleotide SEQ ID
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Wang Z, We
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14-SEP-2000;
19-OCT-2000;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and containing and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and constants.
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                                                peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                   immunosuppressant; cytostatic; gene therapy;
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Xu C, Xue AJ,
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
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                                     Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; cns; partipheral nervous system; cns; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Human polynucleotide SEQ ID NO 853
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Wehrman T, Xu
Goodrich R, I
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2000US-0552317.
2000US-0598042.
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2000US-0662191.
2000US-0693036.
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P-PSDB; AAM39494.
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Wang Z,
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Best Local Similarity:
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19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                   Homo sapiens.
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09-JUL-2000;
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Wang J, V
Zhao QA,
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	gValGlu 	uGlnAla i AGCGGTC	galaLys     GGCTAAT	nGluSer        TGAGTCA	gargser ::: ccaacaa	lyalaн1s GTGGAGGG	lCysHis       GTGTGAT	yLysPro   AAGTGCT	uAspAsp         TGATGAT	pGlyLys         GGGAAAG	rTrpGly TCTGAGC	eGlnGly          CCAAGGA	1Cysser     ATGCAAG	rGlyTyr    ::: GGGATTT	pSerCys           GCAATGT	111eCys         GACATGT	aGlyLys       TGGGACA
rs S	1308-38  (1-1453) x	ValargileHisGluGlnTrpTrpThrileCysAspGlnAsnTrpLysAsnGluGl 	LeuValValCysLysGlnLeuGlyCysProPheSerValPheGlySerArgArgA     :::                 :::::  TCTGTGATTTGTAACCAGCTGGGATGTCCAACTGCTATCAAAGCCCCTGGATGGG	ProSerAsnGlualaArgAspIleTrpIleAsnSerIleSerCysThrGlyAsnGluS.	AlaLeuTrpAspCysThrTyrAspGlyLysAlaLysArgThrCysPheArgArgS: 	LeuvalGl       crGACGCG	SerProcysTyrGlyArgLeuGluValLysTyrGlnGlyGlyThrValCysi:::	AspargTrpSerThrargAsnalaalaValValCysLysGlnLeuGlyCysGlyLysP.     ::::: :: ::   :::   :::	MetHisValPheGlyMetThrTyrPheLysGlualaSerGlyProileTrpLeuAspAsp         :::	ValSerCysIleGlyAsnGluSerAsnIleTrpAspCysGluH1sSerGlyTrpGlyLys:::	HisasnCysvalHisargGluAspvalIleValThrCysSerGlyAspAlaThrTrpGly 	LeuargLeuValGlyGlySerasnargCysSerGlyargLeuGluValTyrPheGlnGly 	ArgtrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaValValCysSer 	GInLeuAspCysProSerSerIleIleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyr 	GlyLysIleTrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCys 	ArgAsnSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAspValGlyValIleCy. ::::::                 ::	SeraspalaSeraspMetGluLeuargLeuValGlyGlySerSerargCysalaGlyLys 
4 13	snAsnCys     -  ACAAGTGT	InAsnTrp	alPheGly :: TCAAAGCC	leSerCys ::       TTTCTTGT	rgThr ::: ATAGTAAC	spLeuArg	lyGluTrp        SACGGTGG	ysGlnLeu ::       GACAACTT	erGlyPro	ysGluHis   ::::     GCAAACAT	ysSerGly        GCTCAAAG	rgLeuGlu            GATTAGAA	ysalaala      ACGATGCT	euGlyAsn      GAGTTAAC	spGluSer     ATGAACCT	erGluAsp ::[       ATGAAGAT	lyserser        GAGGCAGC
Indels: Gaps:	(1-3811) pGlySerA 	eCysAspG :   ::: GTGTAATA	OPheserV   :::: AACTGCTA	eAsnSerI :::: GGATCATG	salaLysa      GGGAAAGC	aAspLeuA ::::   : :CAATTTGG	sTyrGlnG  :::     ATTCCAAG	ValCyst   :::   :  CATTTGTA	sGlualas       aGAAGGCT	eTrpAspC :   :::  cTGGAACT	eValThrC 	sSerGlyA              TTCAGGAA	pasnserI  :::    GGACAGTT	.yMetGlyL :::    :CATTGGTC	saspGlya 	sSerHiss  :::   : caarcaca	uValGlyG   
	AAIS8650 gLeuAlaAs 	TrpThr11    ::	GlycysPr 		ASPGlyLy           GATGGATG	ASPLYSA]      ::  GATGGATC	GluvalLy    :::    GAGATCAP	Alaalava    :::    GCATCTGT	TyrPheLy       AATTTTGG	SerAsnI        TCAGCTC1	ASPValil       GATGCTGG	AsnargCy     ACTGAATC	ASPG1yTr	::: ::: :GTCACAGG	ValSerCy 	ASDASPC) :::       CATTATTC	LeuArgLe              CTAAGACT
41	1453) x A GluLeuArg          GAGCTGAGG	luGlnTrp   :::	ysGlnLeu         ACCAGCTG	laargasp :: :CTGGACGC	ysThrTyr     :::  GCAAACAI	lleCysSer         \CCTGCTCA	lyargLeu       ::: 	Thrargasr ::: NTAGATCAT	SlyMetThr     :::  GTTCATC1	llyasnGlu              GAAATGAG	HisargGlu      ATGCTGAC	SlyGlySer     SATGGAGTC	/alcysasp :::       \TATGTGAT	roserser    :::::	euAspAsp             TTGACAGC	TrpGlyasr           rgggaaa	AspMetGlu    :::     ATCTGGAG
	-381 (1-1 laAspLeuC       CAGACAAGC	rgllehisC :::: \AGTCCAGG	alvalcys!   :::     GATTTGT#	erAsnGlu <sup>1</sup>     TGCAGGT1	euTrpAsp(            TTGGGAT	AspalaGlyvalIleCysSerAspLysAlaAspLeuAspLeuArgLeuValG 	roCysTyrc       GTGTTCTC	rgTrpSer' :::::: ACTTCAAC	isvalPhec Strtcrcrc	erCysile(       argcaac(	snCysVall        \CTGTGATC	rgLeuVald             GACTGGTA	rpGlyThr'             3GGGGACA	euAspCys]            GGGATGTC	yslleTrp)         \CATCTGG	snSerGly': :: ACCATGAAT	spalaser     TGGATCA(
tch	59-130B- 64 GlyAl     22 GGAAC	4 0	04 Leuve     1   2 TCTGT	4 0	4 6	63 Aspa]        22 GATGC	83 SerPi ::: 82 AATAT	03 Aspar      42 GATA	23 MetH1 ::: 02 GTCAC	43 valse ::: 62 CTTA	63 Hisas        22 CATA	83 LeuA3 	m ~	m N	e 0	63 Argas 22 AAAC	83 SerAs        82 TCTG
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01	- U II	5 4	0 0	0 11	٠ .	J 1	<u>ت</u> -	٠ <sub>-</sub>	<b>&gt;</b> 1	<b>&gt;</b> 1	J 1	<b>5</b> 1	٠ <b>-</b>	J 1	~ <b>-</b>	J 1	· -

2141 2261 1721 2021 2201 990 IleHisGlyAsnThrValSerVallleCysThrGlySerLeuThrGlnProLeuPhePro 1009 1961 1010 CysLeuAlaAsnValSerAspProTyrLeuSerAlaValProGluGlySerAlaLeu1le 1029 1030 CysLeuGluAspLysArgLeuArgLeuValAspGlyAspSerArgCysAlaGlyArgVal 1049 GTGTACTCCAAAATCCAGGCAACAAACACATGGCTGTTTCTAAGTAGCTGTAACGGAAAT 1421 GAAACTICTITIGGACTGCAAGAACTGGCAATGGGGTGGACTTACCTGTGATCACTAT 1481 862 882 1782 ACTTGTAGCCACAGCAGGGATGTTGGAGTAGTCTGCTCAAGTAAGACCCAGAAAACATCT 1841 1842 TTAATTGGTTCTTATACTGTGAAAGGGACAGGGTTAGGGAGTCATAGCTGTCTTTTTTTA 1901 949 2081 2262 TGCAATTCATCGTCTTTGGGCCCAACAAGGCCTACCATTCCAGAAGAAGTGCTGTGGCC 2321 929 950 ThrGlyGlyLysTyr11eGlyGluArgSerValArgValTrpGlyHisArgPheHisCys 969 970 LeuGlyAsnGluSerLeuLeuAspAsnCysGlnMetThrValLeuGlyAlaProProCys 989 743 ProHisPheThrGluArgThrLeuHisIleLeuMetSerAsnSerGlyCysThrGlyGly 762 GluAlaSerLeuTrpAspCys1leArgTrpGluTrpLysGlnThrAlaCysHisLeuAsn 782 AspPheSerLeuHisAlaAlaAsnValLeuCysArgGluLeuAsnCysGlyAspAlaIle 842 909 ValGluValAsnValGlnGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGlyMetAsn 722 GlnCysGluGlySerGluThrHisLeuAlaLeuCysProIleValGlnHisProGluAsp AspProGluAspAlaArgValLeuCysArgGlnLeuSerCysGlyThrAlaLeuSerThr 723 IleAlaGluValValCysArgGlnLeuGluCysGlySerAlaIleArgValSerArgGlu 783 MetGlualaSerLeuIleCysSerAlaHisArgGlnProArgLeuValGlyAlaAspMet SerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThrTrpAlaGluLysPhe AspGlyGlnValGluIleAsnValLeuGlyHisTrpGlySerLeuCysAspThrHisTrp 843 930 1362 1662 1722 2202 1242 1302 1422 883 910 703 763 823 863 896 qq qq ò g qq g QQ QQ οy g οy qq ŏ qq ŏ g δ qq ογ g δ ò ò Ωp δλ qq δý g ò q qq οý δ ολ δ ò

-CTTGCAGTTTCCTCAAGAGGAGAAC 3452

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3402 AAAAAGCGAAGACAGAGACAGCGG-
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Query Match:
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                                                                                                                               HisPheGlyGluGlySerGlyProlleTrpLeuAspAspLeuAsnCysThrGlyThrGlu 1109
                                                                                                                                                                            SerHisLeuTrpGlnCysProSerArgGlyTrpGlyGlnHisAspCysArgHisLysGlu 1129
                                                                                                                                                                                                                        AspAlaGlyValIleCysSerGluPheThrAlaLeuArgLeuTyrSerGluThrGluThr 1149
                                                                                                                                                                                                                                                                                                                   ArgAsnIleThrThrAlaIleAlaGlyIleValCySArgGlnLeuGlyCySGlyGluAsn 1189
AlaHisValValCysGlnLysLeuGlyCysGlyValAlaPheAsnAlaThrValSerAla 1089
                                                                                                                                                                                                                                                                    3162 CTCAATGAAGTGAAAGGGAATGAGTTTCCTTGTGGGATTGTCCTGCCAGACGC
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                                   GlulleTyrHisAspGlyPheTrpGlyThrIleCysAspAspGlyTrpAspLeuSerAsp
                                                                                            2442 GCCCACGTGGTTTGCAGACAGCTGGGCTGTGGAAGGCCATTAATGCCACTGGTTCTGCT
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The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as a therosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention are also expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mikita T;
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                                                                                                                                                                                                                                                                                                                                                                                  Human DNA sequence #177 expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
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SerLeuGluGluAsnLeuPheHisGluMetGluThrCysLeuLysArgGluAsp
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Matches:
Conservative:
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The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45139-F45139 and AAB66031-B66057, AAB6604-B66064-B66067-B660657, AAB66064-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-B66067-
                                           Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebroxacular; Alzheiner's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzhelmer's, Parkinson's and Huntington's
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0333159
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Query Match:
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141

LeuArgLeuValAsnGlyAspGlyProCysSerGlyThrValGluValLysPheGlnGly

87

47

28 CysIleLeuLeuLeuAsnSerCysPheLeuIleSerSerPheAsnGlyThrAspLeuGlu

37 TGTGTCTCCTCGGC--

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48

81 67

-----ACCATGGTGGGTGGTCAAGCTCTGGAG

88 GlnLeuGlyCysProPheSerPheAlaMet-----PheArgPheGlyGlnAlaVal 104

GAATGGGGCACAGTGGATGGTTACAGGTGGACATTGAAGGATGCATCTGTAGTGTGCAGA 68 GlnTrpGlyThrValCysAspAspGlyTrpAsnThrThrAlaSerThrValValCysLys

142

⋩	105	HisGlyLys1leTrpLeuAspAspValSerCysTyrGlyAsnGluSerAlaLe	
ą	262	– <u>ڻ</u>	
<u>ک</u> و	125 313	<pre>TrpGluCysGlnHisargGluTrpGlySerHisAsnCysTyrHisGlyGlu 141 :::   :::    :::   </pre>	
<u></u>	142	AspvalGlyvalAsnCysTyrGlyGluAlaAsnLeuGlyLeuArgLeuValAspGlyAsn 161 	
≿.	162	18	
ρ	421	GGACCCTGCTCAGGGCGAGTAGAAGTGCATTCTGGAGAAGCTTGGATCCCAGTGTCTGAT 480	
≿ 4	182	AspGlyTrpAsnLeuAsnThralaAlaValValCysArgGlnLeuGlyCysProSerSer 201 :::            ::::::    :::	
⋩	0	uAspAsp 22	
ą	541	GIGICIGICCIGGACATGAGCICITCAGAGAGICCAGTGCCCAGGTCTGGGCTGAAGAG 600	
≿	222	IleLeuCysGlnGlyAsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTrpGlyAsn 241	
ð	601	TTCAGGTGTGAGGGGGGGGGGGCTGAGCTCTGGGTCTGCCCAGAGTGCCCTGTCCAGGG 660	
ķ	242	HisAspCysSerHisAsnGluAspValThrLeuThrCysTyrAspSerSerAspLeuGlu 261	
ą	661	GGCACGTGTCACCACAGTGGATCTGCTCAGGTTGTTTGTT	
દ્ર વ	262	LeuargLeuvalGlyGlyThrasnargCysMetGlyArgValGluLeuLysIleGlnGly 281     ::                                CTCATGACAAACGGCTCCTCAGTGTGAAGGCAGGTGGAGATGAACAATTCTGGA 777	
⋩	282	ArgTrpGlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaAspValValCysLys 301	
ą	778		
<u>~</u>	302	GlnLeuGlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGlnSerGlySer 321	
ą	838	CAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAGGACCACATTGGTGGAAGAAGGT 897	
≿ q	322	AspvalvalTrpLeuAspGlyValSerCysSerGlyAsnGluSerPheLeuTrpAspCys 341	
≿	342	ArgHisSerGlyThrValAsnPheAspCysLeuHisGlnAsnAspValSerValIleCys 361	
æ	958	CCTGTGACTGCCTGGGTGGTCCTGACTGTTCCCATGGCAACACAGCCTCTGTGATCTGC 1017	
<u>~</u>	362	erAspGlyAlaAspLeuGluLeuArgLeuAlaAspGlySerAsnAsnCysSe	
q	1018	TCAGGAAAC 1026	
≿.	382	GluValArgIleHisGluGinTrpTrpThrIleCysAspGlnAsnTrp	
ð	1027	CAGATCCAGGTGCTTCCCCAG1047	
<u>~</u>	402	lnAlaLeuValValCysLysGlnLeuG	
ð	1048		
<b>≿</b>	422	AlaLysProSerAsnGluAlaArgAspIleTrpIleAsnSerIleSerCysThrGlyAsn 441	
ð	1063	TCTCAACCTACAGGCTCTGCGGCCTCA	
χ.	442	GluSerAlaLeuTrpAspCysThrTyrAspGlyLysAlaLysArgThrCysPheArgArg 461	

QQ	1089	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1089
ΟŸ	462 8	SerAspAlaGlyVallleCysSerAspLysAlaAspLeuAspLeuArgLeuValGlyAla	481
qq	1090	ACAGCGCCCCTACTGCTCAGACAGCAGGCAGCTCCGCTGGT	1143
οy	482 F	HisSerProCysTyrGlyArgLeuGluValLysTyrGlnGlyGluTrpGlyThrValCys	501
qq	1144 0	GTCCCTCCGCCGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTG	1203
δŏ.	502 F	HisAspargTrpSerThrArgasnAlaAlaValValCysLysGlnLeuGlyCysGlyLys	521
QQ	1204	acgeriegeaccregacgargeccegrerererecagecagerage	1263
δλ	522 F	MetHisValPheGly	541
qq	1264 0	CCACGGGTCTGCTCCACGTCGGGCAGGATCAGGGCCCATCTGGTTGGA	1323
οy	542 7	AspValSerCysIleGlyAsnGluSerAsnIleTrpAspCysGluHisSerGlyTrpGly	561
qq	1324 #	TTGAACTGCACAGGAAAGGAGTCCCACGTGTGGAGGTGCCCTTCCCGGGGCTGG	1383
QY	562 I	LysHisAsnCysValHisArgGluAspVallleValThrCysSerGlyAspAlaThrTrp	581
QQ	1384	ZACAACTGCAGACACAAGGAGGCGGGGGGTCATCTGCTCA	1437
Oy	582	GlyLeuArgLeuValGlyGlySerAsnArgCysSerGlyArgLeuGluValTyrPheGln	601
qq	1438 0	SCIGGAAGITITCI	1497
Qy	602 G	GlyArgTrpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaValValCys	621
QQ	1498		1557
Οy	622 8	InLeuAspCysProSerSerIleIleGlyMetGlyLeuGlyAsnAl	640
qa	1558 7	GACAGCTTGGCTGTGGGGACAGTGGAACCCTCAACTCTT	1605
ΟŊ	641 -	TyrGlyLysIleTrpLeuAspAspValSerCysAspGlyAspGluS	657
qa :::	1606	HITTTAGGCCACAGGGTGGATAGAATCCAGTGTCGGAAAACTGG	1665
Οy	658 #	11yTrpGlyAsnAsnAspCysSe	677
QQ	1666 1	creccagretectrecaccerregaatracaacterrecretecraaggage	1725
ογ	678 1	ValGlyValIleCysSerAspAlaSerAspMetGluLeuArgLeuValGlyGlySerSer	269
qq	1726	AGACAGATCCGCCTGGTGGAI	1779
Qy	698 4	ArgCysAlaGlyLysValGluValAsnValGlnGlyAlaValGlyIleLeuCysAlaAsn	717
QQ	1780	GCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGGACCATCTGTGATGA	1839
Qy	718	eAlaGluValValCysArgGln	737
qq	1840 C	credeaccredaccarecccareregrerecaaccaecredecreredaacccr	1899
ογ	738 4	rArgGluProHisPheThrGluArgThrLeuHisIleLeuMe	757
QQ	1900	CCTTCTTCGGGACGGGATCAGGGCCCAT	1959
QY	758 G	rLeuTrpAspCysIleArgT	777
qa	1960 A	AGAGGAGTCCCAAGTATGGAGGTGCCTTCCTGGGGATGGCGG	2019
Qy	778	laHisArgG	197
qq	2020 A	CATCAAGAAGATGCAGGAGTCATCTGCTCAGGATTTGTGCGTCT	2073
Qy	798 v	ValGlyAlaAspMetProCysSerGlyArgValGluValLysHisAlaAspThrTrpArg	817
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                                                                                                    ThrAspValArgLeuVal---AsnGlyLysSerGlnCysAspGlyGlnValGluIleAsn
                                                                                                                                                                                                                                                                                 .GluValPheTyrAsnGlyThrTrpGlySerValGlyArgArgAsnIleThrThrAlaIle
 SerValCysAspSerAspPheSerLeuHisAlaAlaAsnValLeuCysArgGluLeuAsn
                                                                                                                                    GlnHisProGluAspThrCysIleHisSerArgGluValGlyValValCysSerArgTyr
                                                                                                                                                 CCCATCTGGCTGGACGACCTGAACTGCACAGGAAAGGAGTCCCACGTGTGGAGGTGCCCT
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                                            CysGlyAspAlaIleSerLeuSerValGlyAspHisPheGlyLysGlyAsnGlyLeuThr
                                                                  2194 TGTGGCAAGGCTGTGTCTGTCCTGGGACACATGCCATTCAGAGAGTCCGATGGCCAGGTC
                                                                                        TrpAlaGluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCysProIleVal
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                                                                                                                                                                                                                            ACAGACAGAGAGAGACTCCGCCTCAGGGGAGAGAGACAGCGAGTGCTCAGGGCGGGTGGAG
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                                                     LeuSerLysThrGlySerGlyPheMetTrpValAspAspIleGlnCysProLysThrHis
                                                                  GGTCTCAGGGAAGGTTCTAGACCCCGGTGGGTAGATTAATTCAGTGTCGGAAAATGGAT
                                                                                                                                  ACCTCTCTCTGGCAGTGTCCTTCTGGCCCATGGAAATACAGTTCATGCTCTCCAAAGGAG
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GAAGCCTACATCTCATGTGAAGGAAGAAGACCCAAGAGCTGTCCAACTGCTGCCGCCTGC
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         tor cysteine rich domain; SRCR; diagnosis; treatment; medullo-blastoma; glioma; breast; detection;
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                                                                                                 - SRCR protein"
Scavenger receptor cysteine-rich domain
containing protein"
                                                                                                                                                                                                                                                                                                     is containing scavenger receptor, cysteine rich domain for diagnosis and treatment of tumours
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P-PSDB; AAW64591.
           Scavenger receptor
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Best Local Similarity:
Query Match:
                    nervous system; me autoantibody; ss.
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137
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                                                                                                                                                                                                                                                                                                   LeuGlyLeuArgLeuValAspGlyAsnAsnSerCysSerGlyArgValGluValLysPhe 172
                                                                                                                                                                                                                                                                                                                                  TTGGCCCTGAGGCTGGTGAATGGAGGCGACAGTGTCGAGGCCGAGTGGAGGTCCTATAC 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGGCTCCTGGGGCACCGTGTGTGATGACTACTGGGACACCCAATGATGCCAATGTGGTC 919
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  TyrGlyAsnGluSerAlaLeuTrpGluCysGlnHisArgGluTrpGlySerHisAsnCys
                            253 ThrCysTyr-------
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ACCATCACCTTGCATGACAGTAGGATCTGAATCCAGT
LysAlaAspLeuAspLeuArgLeuValGlyAlaHisSerProCysTyrGlyArgLeuGlu                         - TrGGCCTGAGGTGGTGAATGGAGGTGACAGGTGTCAGGGCCCAGTGAA
VallystyrGlnGlyGlufrpGlyThrValCysHisAspArgTrpSerThrArgAsnAla 
AlaValValCysLysGlnLeuGlyCysGlyLysProMetHisValPheGlyMetThrTyr 
PheLysGlualaSerGlyProlleTrpLeuAspAspValSerCyslleGlyAsnGluSer     :::
AsnileTrpAspCysGluHisSerGlyTrpGlyLysHisAsnCysValHisArgGluAsp 
ValileValthrCysSerGlyAspAla
ACCTCACATGCATCAACAGGATCTGAATCCAGTTTGGCCCTGAGGCTGGTGAATGGA
SerAsnArgCysSerGlyArgLeuGluValTyrPheGlnGlyArgTrpGlyThrValCys :::
AspaspGlyTrpasnSerLysalaalavalvalCysSerGlnLeuaspCysProSer 
SerIleIleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyrGlyLysIleTrpLeuAsp :::::: GCCATGTCAGCCCCAGGAAATGCCCGGTTTGGCCAGGGTTCAGGACCCATGTCCTGGAT
AspValSerCysAspGlyAspGluSerAspLeuTrpSerCysÀrgAsnSerGlyTrpGly
AsnàsnàspcysSerHisSerGluaspValGlyValIleCysSer
CCGACACCCAGCCCAGACACTTGGCCAACCTCACATGCATCAACAGGAGGATCTGAATCC
AspMetGluLeuArgLeuValGlyGlySerSerArgCysAlaGlyLysValGluValAsn :::
ValGingiyalaValgiyileLeuCysAlaAsnGiyTrpGiyMetAsnIleAlaGiuVal:::   :::   :
ValCysargGlnLeuGluCysGlySeralaIleargValSerargGluProHisPheThr 
GluArgThrLeuHisIleLeuMetSerAsnSerGlyCysThrGlyGlyGluAlaSerLeu

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6 6	3404 AACTGTGGCCATCACGAAGACGCTGGTGTCATCTGCTCAGCCACCCAAATA 3454	KW	respiratory diseas
òá	1144 TyrSerGluThrGluThrGlu 1150	X O X	Homo sapiens.
,	SerCysAlaGlyArgLeuGluValPheTyrAsnGlyThrTrpGlySer	T. E.	CDS
a &	} }	XX NG X	WO200179454-A1.
ු යු	3569 CCTGCATACTACCCCAACAATGCTAAGTGTTTGGGAAATAGAAGTGAATTCTGGTTAT 3628	Od X	
Qy Dp	1167ValGlyArgArgAsnIle	Y X Y Y	11-APR-2001; 2001 13-APR-2000; 2000 24-APR-2000; 20000
oy Ob	1173	X P P X	
oy Op	1182AlaPro 1196 1184AlaPro 1196 1199 GATACCAGGCAAATATTACATCTTACAACGAATGACCATTCACTTTCGAAGTGAC 3808	PI XX DR DR	Agarwal P, Murdoo WPI; 2002-061975/C P-PSDB; AAU09878.
Oy Op	1197 LeuSerLysThrGlySerGlyPheMetTrpValAspAspIleGlnCysProLysThr 1215 	XXLLL	New secreted prote autolumune disease disorders, inflamm
9 9	1216 HisileSerileTrpGlnCysLeuSerAlaProTrpGluArgArgIleSerSerProAla 1235 		Claim 2; Page 47-4 The invention rela
Oy Dp	1236 GluGluThrTrpIleThrCysGluAspArgIleArgValArgGlyGlyAspThrGluCys 1255 	8888	polynucleotide (II autoimmune disease disorders, inflamm psychiatric diseas
oy ea	1256 SerGlyArgValGluIleTrpHisAlaGlySerTrpGlyThrValCySAspAspSerTrp 1275 :::	8888	renal diseases, or treat diseases, ak expression, produc vaccines for induc
Qy Db	1276 AspLeuAlaGluAlaGluValValCysGlnGlnLeuGlyCysGlySerAlaLeuAlaAla 1295 :::	8888	uct mmu
O O	1296 LeuargaspalaserPheGlyGlnGlyThrGlyThrIleTrpLeuaspaspMetargCys 1315     :::	8888	may be used as dia and in tissue exploading sequence of
O O	1316 LysGlyAsnGluSerPheLeuTrpAspCysHisAlaLysProTrpGlyGlnSerAspCys 1335 	SQ . Alig	<pre>SQ Sequence 2697 BP; Alignment Scores: Pred. No.:</pre>
6 G	1336 GlyHisLysGluaspalaGlyValargCysSerGlyGlnSerLeuLysSer 1352 	Score: Percen Best L	Score: Percent Similarity: Best Local Similarity: Query Match:
RESULT AAS1759	13	- SD - CO	US-09-759-130B-381 (1-
Z X X X	AAS17590;	do .	536 GlyProlleTrpl        :: 31 GGGCCCTTCTT
T X E	26-FEB-2002 (first entry)	Qy	556 GluHisSerGly
XX	cytostatic: immunosuporessive:	qa 	61 CCCATTGGTGGA
K.	sectored process, cycoscatte; immunosuppressive; varietary; vacture; antiinflammatory; neuroprotective; nephrotropic; cardiovascular;		576 SerGlyAspAla

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relates to an isolated novel secreted polypeptide (I) and (II). (I) and (II) are useful for treating cancer, Iseases, wound healing disorder, infections, hematopoletic filammatory disorders, infertility, neurological and iseases, cardiovascular diseases, respiratory diseases, cardiovascular diseases. These may also be used to ss, an organities and disorders caused by abnormal production, function and/or metabolism of the genes, as inducing immunological response in a mammal, and in those for detecting the effect of added compounds on the mRNA and polypeptide in cells. The polypeptides can be used s to produce antibodies immunospecific for the polypeptides, it membrane-bound or soluble receptors. The polypeptides is standardior studies, in chromosome localisation studies, is expression studies. The present sequence represents the ce of novel human secreted protein #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 teins or polypeptides, useful for treating e.g. cancer, ses, wound healing disorder, infections, haematopoietic mmatory disorders, infertility, cancer
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utoimmune disease; wound healing disorder; infection; isorder; inflammatory disorder; infertility; ease; psychiatric disease; cardiovascular disease; ase; renal; gastrointestinal; ss.
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361
108
262
219
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Matches:
Conservative:
Mismatches:
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NE BEECHAM PLC.
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OUS-199417P.
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<b>~</b> 0	596	LeuGluvaltyrPheGlnGlyArgTrpGlyThrValCysAspAspGlyTrpAsnSerLys 615 	
<b>&gt;</b>	616	aAlaAlaValValCysSerGlnLeuAspCysProSerSerIleIleGlyMetGlyLeu 6	
o >-	989	sp 65	
۵	241	GTCCCGCTGCAGAGAGATGGCCCAGCCTGGCTTCACAACGTGTCCTGCCGGGGCAAC 300	
م ح	301	GluseraspLeuTrpSerCysArgAsnSerGlyTrpGlyAsnAsnAspCysSerHisSer 675 	
2 م	676 361	GluaspvalGlyvalIleCysSerAspAlaSerAspMetGluLeuArgLeuValGlyGly 695	•
<b>λ</b> Ω	696	SerSerArgCysAlaGlyLysValGluValAsnValGlnGlyAlaValGlyIleLeuCys 715 	
۵ ہ	716	AlaAsnGlyTrpGlyMetAsnIleAlaGluValValCysArgGlnLeuGluCys 733 ::::::::	
>- Q	734	GlySeralaileargValSerArgGluProHisPheThrGluArgThrLeuHisIleLeu 753	
γ Q	754	31yGluAlaSer  +  accGAGCCCACC	
ъ Q	774	TrpLysGlnThralaCysHisLeuAsnMetGluAlaSerLeuIleCysSerAlaHisArg 793 :::::	
y .d	794	GInProArgLeuValGlyAlaAspMetProCysSerGlyArgValGluValLysHisAla 813 :::               :::       :::	
y d	814	ASPThrTrpArgSerValCysAspSerAspPheSerLeuHisAlaAlaAsnValLeuCys 833          :::            - ACCTGGGGACCGTCTGTGATGCGGCCCTGGACCTGGCCACGCCGCGTGTGTGC 798	
γQ	834	ArgGluLeuAsnCysGlyAspAlaIleSerLeuSerValGlyAspHisPheGlyLysGly       853	
ъ q	854 859	AsnGlyLeuThrTrpAlaGluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeu 873 :::	
ь ч	874 919	Val 8	
γq	894 973	CysSerArgTyrThrAspValArgLeuValAsnGlyLysSerGlnCysAspGlyGlnVal 913         :::	
y d	914 1024	GlulleĄsnValLeuGlyHisTrpGlySerLeuCysAspThrHisTrpAspProGluAsp 933 	
Α.	934	AlaargValLeuCysargGlnLeuSerCysGlyThrAlaLeuSerThrThrGlyGlyLys 953	

qq	1084	GCCACCGICCICTGCCACCAGCICAACIGIGGCAACGCGGIGGCCGCACCIGGAGGAGGC 1143
Qy	954	yrileglygluArgSerValArgValTrpGlyHisArgPheHisCysLeuG
Dp	1144	GGACGGGACGCTGCCATCTGGCCTGATGCCTTTCACTGTGAGGGACAGA
ΟŊ	974	
QQ	1204	GTGCCCGGGAAA
oy d	994	ThrvalServalIleCysThrGlySerLeuThrGlnProLeuPheProCysLeuAlaAsn 1013
a ò	o ~	ValProGluGlySerAlaLeulleCysLeuGluAsp 103
- qa	1297	
δλ	1034	ArgLeuArgLeuValAspGlyAspSerArgCysAlaGlyArgValGluIl
qa .	1300	CTGCGACTGAGGGAAGGACAGAGCCGCTG
QY	1051	1051
qq	1354	GATGGCGTGTGGGGCCGCCTCCTGGACGATGCCTGGGACCTGCGCGCGC
Qy	1051	1051
Ob	1414	TGCCGGCAACTCGGGTGCAGAGGGGCCCAGCAAGCCTATGACGCACCTGCCCCCAGCCGC 1473
δλ	1051	1051
qq	1474	GGATCCGTCCAGGTGGCGCTGAGCCGCTGTGCTGGGCACCGAAACCCGCCTGACT 1533
Qγ	1051	1051
qq	1534	CAGTGCAACGTGTCCGCGACCCTGCAGGAGCCCGCGGGGACCTCGCGGGACGCCGGCGTG 1593
Qy	1051	1051
qq	1594	GTGTGCTCCGGTGAGGTCGGAACCGCGTCCCCCATGGCCCGTCGCCACGGGATCCCGGGC 1653
δy	1051	1051
qq	1654	GCCCTGACTCTGTCTCTCCACAGGGAGCCTCAGGGTGCGGCTGGCCGCGGGGGCCGGGGCC 1713
Οy	1052	TyrHisAspGlyPheTrpGlyThrIleCysAspAspGlyTrpAspLeuSerAspAlaHi
QQ	1714	CTGCACGGGGGCGCGTGGGGCACCGTGTGTGATGCCTGGGACCTGCGGGACGCGCAC 1773
Qy	1072	ValValCysGlnLysLeuGlyCysGlyValAlaPheAsnAlaThrValSerAlaHisPhe 1091
QQ	1774	GTGGTCTGCAGGCAGCTGGGCTGTGGCCGCGCCCTGAGCGCCCCTGGGGGCCCGCACTT
Qy	0	GlyGluGlySerGlyProlleTrpLeuAspAspLeuAsnCysThrGlyThrGluSerHis 11
Q O	e e	GGAGCCGGGGCAGGGCGCATCTGGCTGGACGAGCTGCCAGGGCCAGGGCCACGAGTCTGCG 189
ΟŊ	$\vdash$	LeuTrpGlnCysProSerArgGlyTrpGlyGlnHisAspCysArgHisLysGluAspAla 113.
qq	6	CTGTGGCAGTGCCCGTCGGCGGGCTGGGGGCGGCACGACTGGAGGCACAAGGAGGACGCC 195
ΟŊ	3	GlyvallleCysSerGluPheThrAlaLeuArgLeuTyrSerGluThrGluThrGluSer 11
qq	1954	GGCGTCTTCTGCTCAGAGTCGGTGGCTCTGAGGCTGCGAGGTGGGACCTGCTGC
QY	15	CysAlaGl
an	3	TGTGCTGGGTGGGCTGGGCGTGTTCTACAATGGGGGCGCCCCATGGGGCGCCACAACAACAACAACAACAACAACAACAACAAC
δλ d	1172	IleThrThrAlaIleAlaGlyIleValCysArgGlnLeuGlyCysGlyGluAsnGlyVal 1191

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Human; mouse; xenopus; rat; secreted expressed sequence tag; SEST;

wexpressed sequence tag; EST; probe; chemotractic; proliferative;

mimunomodulatory; haematopoletic; chemotinetic; analgesic; haemostatic;

mimunomodulatory; haematopoletic; chemotinetic; analgesic; haemostatic;

which is antidial antidial antistimatory; cytostatic; antibacterial; antifungal;

mitulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian;

mitulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian;

merebroprotective; anticonvulsant; antidepressant; gene therapy;

vaccine; autoimmune disorder; multiple sclerosis; allergic condition;

minsulin dependent diabetes; asthma; meloid cell deficiency; ulcer;

mynphoid cell deficiency; burn; osteoporosis; osteoarthritis;

central nervous system disorder; Alzheimer's disease; stroke;

mynphoid sideses; Hunington's disease; conqulation disorder;

mynphoid antimour; infection; depression; psoriasis; ss.
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                                                                       AspIleGlnCysProLys---ThrHisIleSerIleTrpGlnCysLeuSerAlaProTrp 1227
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                                                                                                       2185 AACATGGAGGCGGCAGGCTGCCCAACTCCACTCTGTGGCAATGCCCTTCCCACGTGG
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 ValSerLeuAla-
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AAA41261 to AAA43419 represent specifically claimed secreted expressed sequence tags (SESTS), isolated from human, mouse, xenopus and rat tissue sources. The SESTS can have a range of activities depending on the tissues they were isolated from. The activities include: the tissues they were isolated from. The activities include: chemokinetic; analgesic; haemostatic; thrombolytic; antidiabletic; chemokinetic; antipacterial; antidiadal; antidiabletic; cytostatic, antipackinsonian; antipsoriatic; cerebroprotective; cototropic; antipackinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The SESTS can be used for gene therapy and in vaccines. The SESTS are useful as probes for the identification and isolation of full-length conversed by the SESTs centibodies. They may be useful for treament of autoimmune disorders are useful in assays for determining biological activity and raising are useful in assays for determining biological activity and raising are useful in assays for determining biological activity and raising (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (cathma) myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, parkinson's, Huntington's disease, stroke), coagulation diseases, tumours, bacterial, fungal or viral infections, depression and psoriasis. AAAA43420 to AAA43425 represent invention.
                                                                                                       Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 ralaSerThrValValCysLysGlnLeuGlyCysProPheSerPheAlaMetPheArgPh 100
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               ن
                 Evans
               Collins-Racie LA,
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Matches:
Conservative:
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               LaVallie ER,
                                                                                                                                                                                 Claim 1; Page 527; 618pp; English.
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1404.00
96.98%
95.47%
17.25%
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Query Match:
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Merberg D,
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antialiflammatory; antirheumatic; antiarthritic; immunosuppressive; antianterizal; endocrine; cardiant; cartiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antiant-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiagregant; haemostatic; unterary; antiulcer; osteopathic; eczema; demarchological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuropathogostal; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; allergic rhunitis; diabetes; multiple sclerosis; depression; allergic rhunitis; diabetes; multiple sclerosis; depression; Alzhelmer's disease; parkinson's disease; neurodegenerative disorder;
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|AAACAC-TCCTGTTCAGGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGAACTATATG
                                                                                                                                                                           sAspAspGlyTrpAsnLeuAsnThrAlaAlaValValCysArgGlnLeuGlyCysProSe
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                                              yGluAspValGlyValAsnCysTyrGlyGluAlaAsnLeuGlyLeuArgLeuValAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein encoding cDNA sequence SEQ ID NO:93
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2000US-0488725.
2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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21-JAN-2000;
25-APR-2000;
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AAM25965 to AAH99904 encode the human proteins given in AAM25255 to
AAM25963. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antinflammatory; antisheumatic;
central they are expressive; antibacterial; endocrine; cardiant;
central nervous system; virucide; anti-HIV; fungicide; antimutagen;
cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
antiplorarinsonian; and immunostimulant. The proteins and polynucleotides
antiplarkinsonian; and immunostimulant. The proteins and polynucleotides
conciding them can be used in gene therapy, antisense therapy and vaccine
production, The proteins and polynucleotides are useful for screening for
agonists or antagonists of a protein and for the treatment and diagnosis
of disorders associated with the activity of a protein e.g. inflammation,
rheumatoid arthritis, septic shock, pancreatifis, cardiac dysfunction,
neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
infections, autoimmunity, genetic diseases, hemmatopoietic disorders,
anaemia, platelet disorders, thrombooytopaenia, wounds, burns, ulcers,
costeoporosis, severe combined immunodeficiency, cardiac,
costeoporosis, severe combined immunodelians.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoporosis, severe combined immunodeficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depressi
Alzheimer's disease, Parkinson's'disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 690 BP; 163 A; 134 C; 207 G; 186 T; 0 other;
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Mismatches:
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                                                                                       treatment and diagnosis of e.g. cancer,
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99.07%
99.07%
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2001-457603/49.
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Best Local Similarity:
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Search completed: May 12, 2003, 06:58:24 Job time : 670 secs

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 999)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL529439 ALI_NFL001_NBC4 Homo sapiens cDNA clone CSODD006YO05 5
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AL529438
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AUTHORS
TITLE
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KEYWORDS
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-Cgn2_1/USPTO_spool/US09759130/runat_06052003_123554_23365/app_query.fasta_1.1607
-DEV_CGn2_1/USPTO_spool/US09759130/runat_06052003_123554_23365/app_query.fasta_1.1607
-DEV_CGn2_10_-TEV_CGNE_PCT_-TRN_MAY_LON_-TRANS=human40.cdi -LIST-45
-UORINGN=200 -THR_SCORE=PCT_-THR_MAX=100 -THR_MIN-0. ALIGN=15 -MODE-LOCAL
-UOSER-US09759130_eCGN_1_12168_erunat_06052003_123554_23365 -NCFU=6 -ICPU=3
-NO_ALREY -NO_MARP_-LARGEQUERY - NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=12
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AK014331 Mus muscu B1036644 IL3-NT028 B16308 34707.TP CI B0327933 MR4-RT004 BC035470 Homo sapi BG534729 602553892

MR4-RT004 MR4-RT004

BQ936228 AGENCOURT AL570629 AL570629 BF096204 MR3-UT009

MR4-RT004

MR4-RT004

AGENCOUR

AL529438 AL529438 BI838644 603086185

BI183796 UNL-P-FN-

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AL529439 AL529439

Description

SUMMARIES

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AL540904 AL540904

4-RT004

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BI009799 MR4-RT004

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pg11c.pk0 PM3-GN051

AV616074

BC020481 Homo sap: AL550308 AL550308

ALIGNMENTS

BF792807 BC020481 BQ368412

MR4-RT00

EST 13-FEB-2001

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cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http:/fullength.invitrogen.com"
10 a 236 c 318 g 224 t 1 others
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web
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enriched, double-stranded-cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcWNSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : filang@ilfetech.com URL :
http://fulllength.invitrogen.com"
3 others
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 940)

S Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

L Onpublished (2001)

Contacti Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqrefégenoscope.cns.fr.

Location/Oullifiers

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AL50994.1 GI:12888516
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GlyCysGlyValAlaPheAsnAlaThrValSerAlaHisPheGlyGluGlySerGlyPro 1097
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BG570972 582 bp mRNA linear EST 10-APR-2001 602591546F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4714115 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
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TAG_SEQ=None
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Best Local Similarity:
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/clone_lib="UNL-P-EN-wa-01-0-UNL"
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/dev_stage="ADDLT"
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polylinker; Site_l: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. Seq primer: M13 -29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The library was constructed as described on and Soares, Genome Research 6: 791-806
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Caetano, A.R., Johnson, R.K. and Pomp, D. Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles
Unpublished (2001)
                                                                                                                                         1248
                                                                   AspileGlnCysProLysThrHisIleSerIleTrpGlnCysLeuSerAlaProTrpGlu 1228
                                                                                                                                                                                                                                                                                 ThrValCysAspAspSerTrpAspLeuAlaGluAlaGluValValCysGlnGlnLeuGly 1288
AsnGlyValValSerLeuAlaProLeuSerLysThrGlySerGlyPheMetTrpValAsp 1208
                                  301
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                    ArgGlyGlyAspThrGluCysSerGlyArgValGluIleTrpHisAlaGlySerTrpGly
                                                                                                                                                                                                                              ACAGTGTGTGATGACTCCTGGGACCTGGCCGAGCCGGAAGTGGTGTCAGCAGCTGGGC
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BI185454
BI185454.1 GI:14659863
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 66583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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/clone_lib-"LT_FE002_PL1"
/lab_host-"DH10B"
/note-"Organ: placents, Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL540905 LIL_FL002_PL1 Homo sapiens cDNA clone CSODE004XI19 5 prime
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1100)
14, W.B., Catuber, C., Jessee, J. and Polayes, D.
Full: Tength CDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                   900 TTCCAAGGAGAATGGGGGACAATATGTGATGACGCCTGGGACAGTTACGATGCTGCTGTG 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 ValCysLysGlnLeuGlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGln 318
 AspGlyAsnAsnSerCysSerGlyArgValGluValLysPheGlnGluArgTrpGlyThr 178
                                                                                                                                                                                                              179 IleCysAspAspGlyTrpAsnLeuAsnThrAlaAlaValValCysArgGlnLeuGlyCys 198
                                                                                                                                                                                                                                  199 ProSerSerPhelleSerSerGlyValValAsnSerProAlaValLeuArgProIleTrp 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               780 PGGGGAAAGCATAACTGTGATGCTGAGGATGCTGGAGTGATTTGCTCAAAGGGAGCA 839
                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpGlyAsnHisAspCysSerHisAsnGluAspValThrLeuThrCysTyrAspSerSer
                                                                                           180 CACCAACAAGATGCTGGAGTGACCTGCTCAGATGGATCCAATTTGGAAATGAGGCTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 IleGlnGlyArgTrpGlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaAspVal
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                                                           HisGlyGluAspValGlyValAsnCysTyrGlyGluAlaAsnLeuGlyLeuArgLeuVal
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODE004Y119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , mRNA sequence.
AL540905
AL540905.1 GI:12871463
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KEYWORDS
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TITLE
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/db_xrefe"taxon:9606"
/clone_inbe_rCSDIO21xH23"
/clone_libe_rITI_NFL06_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/clone_libe=rITI_AFL06_PL2"
/tissue_type="placenta"
/note="Wector: pCWNSPORT 6; Site_l: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filanglifetech.com URL: http://fullength.invitrogen.com"

http://fullength.invitrogen.com"
AL544534 LII_NFL006_PL2 Homo sapiens cDNA clone CS0D1021YH23 5
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Joses 1 to 1108)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Uni,W.B., Gruber,C., Jessee,J. and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualiflers
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                                                                           AL544534.1 GI:12877014
                                 prime, mRNA sequence.
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942.50
65.58%
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Best Local Similarity:
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                                                     AL544534
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                                                                                                                                                                                                          AUTHORS
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718 bp mRNA linear EST 10-JUL-2001
UNL-P-FN-cd-h-08-0-UNL.sl'UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-cd-h-08-0-UNL.3', mRNA sequence.
                                                                                                                                                                               299 ValCysLysGlnLeuGlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGln
                                                                                 908 TTCCAAGGAGAATGGGGGACAATATGTGATGACGCTGGGACAGTTACGATGCTGCTGTG
                                                                                                                                               968 GCATGCAAGCAACTGGGATGTCCAACTGCCGTCACAGCCATTGGTCGAGTTAACGC-MRT
                                                 279 IleGlnGlyArgTrpGlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaAspVal
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and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
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50.15%
11.51%
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Euteleostomi;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1 (bases 1 to 718)
Caetano, A.R., Johnson, R.K. and Pomp, D.
Generation and sequence characterization of a normalized cDNA
Library from swine ovarian follicles
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Oligo-dr track not found, Not I si
is likely internal to the message.
Seq primer: M13 -29
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Department of Animal Science,
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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Catarrhini; Hominidae; Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 554)
Li,W. B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Mismatches:
Indels:
   Length:
Matches:
                                                                      US-09-759-130B-381 (1-1453) x BI183796 (1-718)
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AL529438 LTI_NFL001_NBC4
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AL529438.1 GI:12792931
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AUTHORS
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JOURNAL
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//lab_host="DH108"
//note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized Library was constructed by Life Technologies, contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fullength.invitrogen.com"
13 a 166 c 127 g 110 t 19 others
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                                       : www.genoscope
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Mismatches:
Indels:
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Matches:
Genoscope - Centre National de Seque
BP 191 91006 EVRY cedex - France
Email: segrefêgenoscope cns.fr, Web
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                                                        Location/Qualifiers
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895.00
90.81%
88.65%
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361

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1039 lAspGlyAspSerArgCysAlaGlyArgValGluIleTyrHisAspGlyPheTrpGlyTh
                                                                                                                                   182 TCAGGAAACCAGTCCCAAACACTGTCCTCGTGCAATTCATCGTCTTTGGGCCCAACAAGG
                                    1020 SerAlaValProGluGlySer-AlaLeuIleCysLeuGluAspLysArgLeuArgLeuVa
                                                         242 CCTACCATTCCAGAAGAAACGTGCTGTGGCCTGCATAGAGAGTGGTCAACTTCGCCTGGT
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AL540904/c
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fordy-SpoRT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(ECORV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code C. 274 g 213 t
                                                                                          930 bp mRNA linear EST 04-OCT-2001
Homo sapiens cDNA clone IMAGE:5225205 5',
                                                                                                                                                                                                                                                                                                                              Dupublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Phe I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM1156 row: j column: 22
High quality sequence stop: 731.

Location/Qualifiers
                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                              1 (bases 1 to 930)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_120"
/lab_host="DH10B"
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BI838644.1 GI:15950194
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Best Local Similarity:
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AUTHORS
TITLE
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AL540904 LTL_FL002_PL1 Homo sapiens cDNA clone CSODE004XI19 3 prime
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedèx - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        1099 rpLeuAspAspLeuAsnCysThrGlyThrGluSerHisLeuTrpGln-CysProSerArg
                                                                                                                                                                                                                                   1139 ThrAlaLeuArgLeuTyrSerGluThrGluThrGluSerCysAlaGlyArgLeuGluVal
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     rlleCysAspAspGlyTrpAspLeuSerAspAlaHisValValCysGlnLysLeuGlyCy
                                                                                                                                  602 ATGTCTCTGAGACTGACCAGTGAAGCCAGGAGAGGCCTGTGCAGCCGTCTGGAAGTT
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Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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892 TGACTCACATGTGACACAGAATACAATCAAGAAGGC 927
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US-09-759-130B-381 (1-1453) x BI836459 (1-723)
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/clone="cs0bE0047119"
/clone=lb="LTI_FL002_PL1"
/lab_host="DH10B"
/note="organ: placenta; Vector: pCMVSPORT 6; 1st strand
/note="organ: placenta; Vector: pCMVSPORT 6; 1st strand
/note="organ: placenta; Vector: pcMVSPORT 6; 1st strand
cDMA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
/ Maryland 20850, USA Fax : (1) 301 610 8371 Email :
filangeilifetech.com URL :
http://fullength.invitrogen.com"
http://fullength.invitrogen.com"
a 300 c 228 g 313 t 20 others
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Matches:
Conservative:
Mismatches:
Indels:
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767.00
65.45%
48.50%
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Best Local Similarity:
Query Match:
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qq	493	GCATTATTCTTCTTGACTAAAAAGCGAAGACAGAGACAGCMSCTTGCAGTT 443
οy	1396	SerThrargargargalySerLeuGludludsnLeuPheHisGluMetGluThrCysLeu 1415
qq	442	CCCCCAAGGAGAGAGAACTTAGTCCACCAAATTCAATACCGGGAGATGAANTCTTGCCTG 383
OY	1416	rPro
qa	382	AAKGCAGATGATCTGGACCTAATGAATTCCTCAGAAAATTCCCATGAGTCAGCT 329
QY Db	1436	AspalaseraspThrSerLeuLeuGlyValLeuProalaserGlualaThr 1452 
ò	-	
경 검		266
RE LOC	RESULT 11 B1836459 LOCUS DEFINITION	-
A VE	ACCESSION VERSION KEYWORDS	sequence. 159 159.1 GI:15948009
OS -	SOURCE ORGANISM	human. Homo sapiens Enkarvota: Metazoa: Chordata:
RE	REFERENCE	Mammaljou, Marchas Primates; Catarrhini; Hominidae 1 (bases 1 to 723)
	AUTHORS TITLE	
CO	COMMENT	outputished (1999) Contact: Robert Strausberg, Ph.D. Email: cranbs-r@mail nih cov
		Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
		DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNY at:
		http://image.llnl.gov Plate: LLAM11558 row: a column: 10
FE	FEATURES	
	T C C	
		/clone="IMAGE:5221905" /clone_lib="NIH_MGC_120" //ab host="nH1DMC_120"
		/note="Organ: pooled pancreas and spleen; Vector: pcMv-SPORT6; Site_1: Not1; Site_2: EcoRv (destroyed); RNA
		source anonymous pool of spleen and pancteas from 28 yo male. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning)   Average insert
		insert size range la d enriched for full C. Gruber (Invitro
BA	BASE COUNT ORIGIN	173 a
. Al	Alignment Pred. No.:	Scores: 5.24e-64 Length:
	Score: Percent Si Best Local Query Matc	Score: 739.00 Matches: 144 Percent Similarity: 73.88% Conservative: 37 Mismatches: 54 Query Match: 9.08% Indels: 10 DB: 13 Gaps:
ns	-09-759	11836459

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Percent Similarity:
Best Local Similarity:
Query Match:
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1 (bases 1 to 644)

2 (bases 1 to 644)

2 (bases 1 to 644)

2 (bases 1 to 644)

3 (bases 1 to 644)

3 (bases 1 to 644)

4 (bases 1 to 644)

4 (bases 1 to 644)

5 (bares 1 to 644)

6 (bases 1 to 644)

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MR4-RI0048-170401-008-b11 RT0048 Homo sapiens CDNA, mRNA sequence.
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                                                                                                         1049
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                                                   61
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1010 CysLeuAlaAsnValSerAspProTyrLeuSerAlaValProGluGlySerAlaLeuIle
                                                                                                                                                                                                                                                                             122 GAGATCTATCATGAGGGCTCCTGGGGCACCATCGTGTGATGACAGCTGGGACCTGAGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 GAAGTCCCGCATTTGGCAGTGCCATTCACACGGCTGGGGGCCAGCAAAATTGCAGGCACAA
                                                   2 recaarrearcerettresseceaacaassecrascarrecasaasaasresressec
                                                                                                            1030 CysLeuGluAspLysArgLeuArgLeuValAspGlyAspSerArgCysAlaGlyArgVal
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Proc. Ntl. Acad. Sci. U.S.A. 97 (7), 3491-3496-(2000)
20202663
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Laboratory of Cancer Genetics
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BI009838.1 GI:14413909
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="Rr0048"
/dev.stage="Adult"
/note="Organ: Kidney_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                Fax: +55-11-2707001
Email: asingpsom@ludwig.org.br
Email: saingpsom@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR4st2=MR4-RT0048-
170401-008-blist5=2001-04-17st4=1)
Seq primer: puc 18 forward
High quality sequence start: 33
High quality sequence start: 33
High quality sequence stores: 538.
                     Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 AGTAGCATGTCTGAAACCACTGTGGGTGTGGTGTGCAGCAGCTGGGCTGTGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 GAAGGACCCACTTCCTGTTCTGGACGTGTGGAGATCTGGCATGGAGGTTCCTGGGGGACA
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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718.00
79.90%
62.37%
8.82%
                                                                        Tel: +55-11-2704922
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DEFINITION ACCESSION

ORGANISM

KEYWORDS

VERSION SOURCE REFERENCE AUTHORS

RESULT 13 BQ327934 LOCUS

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Email: cgapbs-remail.nl. gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Parayad by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BES02724 1653 bp mRNA linear; EST 04-AUG-2000 hz78d12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone iMAGE:3214103 3' similar to TR:Q07898 Q07898 M130 ANTIGEN PRECURSOR; ;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 653)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                           GluAsnGlyValValSerLeuAlaProLeuSerLysThrGlySerGlyPheMetTrpVal 1207
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1148 GluThrGluSerCysAlaGlyArqLeuGluValPheTyrAsnGlyThrTrpGlySerVal 1167
                                                                                                                                                                                                      422 GGGACAGTGTGTGATGACTCTTGGGACGTTGGACGATGCTCAGGTGGTGTGTGACAACAACTT 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seg primer: -400r 110m older High quality sequence stop: 483
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4st2=MR4-RT0048-070501-010-g04st3=2001-05-07st4=1)
Seq primer: puc 18 forward
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//dev.stage="Adult"
//dev.stage="Organ: kidney_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                        BQ327934 585 bp mRNA linear EST 17-MAY-2002
MR4-RT0048-070501-010-904 RT0048 Homo sapiens CDNA, mRNA sequence.
BQ327934
                                                                                                                                                                                                                                                                                                                                                                                          Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balia,G.S., Simpson,D.H., Brunstein,A., Geoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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High quality sequence stop: 584
Location/Qualifiers
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Fax: +55-11-2707001
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source

FEATURES

JOURNAL MEDLINE COMMENT

TITLE

BASE COUNT

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Score:

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/note="Organ: Kidney_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under 10m stringency conditions.
                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 616)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silvay,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LiCR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/soripts/gethtml2.pl?tl=MR4&t2=MR4-RT0048-
170401-007-b01&t3=2001-04-17&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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/dev_stage="Adult"
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High quality sequence stop: 615.
Location/Qualifiers
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Fax: +55-11-2707001
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                /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCL_CGAP_LuS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-14179) and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CysSerGlyArgValGluValLysHisAlaAspThrTrpArgSerValCysAspSerAsp
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Conservative: Mismatches: Indels: Length: Matches:

Gaps:

Search completed: May 12, 2003, 17:31:28 Job time: 2883 secs

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Perfect score:

Title:

Sequence:

OM protein

Run on:

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TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.1
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Mismatches:
Indels:
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US-08-794-795-1

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US-09-214-278-4

US-08-813-214-21

US-09-214-278-4

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CS-09-467-997-6

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US-08-718-388-6

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Patent No. 6346606
GENERAL INFORMATION:
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US-09-341-587-4
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Best Local Similarity:
Query Match:
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          GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                              nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                               of hits satisfying chosen parameters:
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                                                                                                                                                                                              441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Database

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	m m	1 PhealaglyLeuProHisLeuGlnSerGlySerAspValValTrpLeuAspGlyValS	31
	. ⊢ დ	1 TrpAsnAsnAlaAlaAsaPValValCysLysGlnLeuGlyCysGlyThrAlaLeuHi    ::: :::    :::	29
σ	290 127	1 CysMetGlyArgValGluLeuLysIleGlnGlyArgTrpGlyThrValCysHisHisLys	27
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o.	252	3 ASOCYSArgHisArgGlyTrpGlyAsonHisAspCysSerHisAsoGluAspValT :::	23
σ	232	3 ValleuArgProileTrpLeuAspAspileLeuCysGlnGlyAsnGluLeuAlaLeuTrp	21
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	172 859	3 LeuGlyLeuArgLeuValAspGlyAsnAsnSerCysSerGlyArgValGluValLysPhe	15
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	148 739	8 TyrhisGlyGluAspValGlyValAsnCysTyr	13
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	117 619	<pre>PheArgPheGlyGlnAlaValThrArgHisGlyLysIleTrpLeuAspAspValSerCys                                      </pre>	56.9
	97 568	1 AlaSerThrValValCysLysGlnLeuGlyCysProPheSerPheAlaMet :::          :::	50
	508	9 GIGGAGAICCIAIACCGAGGCICCIGGGGCACCGIGIGIGAIGACAGCIGGGACACCAAI	44

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qq	1691	cercrecaeccaeccesecrerescocarercaecc
δy	531	eGlyAsnGluSer 550
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Qy	589	SerAsnArgCysSerGlyArgLeuGluValTyrPheGlnGlyArgTrpGlyThrValCys 608
Ob	1991	GTGT
QY	609	spAspGlyTrpAsnSerLysAlaAlaAlaV
qq	2051	- [5
δλ	629	SerileileGlyMetGlyLeuGlyAsnAlaSerThrGlyTyrGlyLysileTrpLeuAsp 648
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Qy	687	n 706
qq	2351	AGGTGACAGGTGTCAGGGCCGAGTGGAGGT

	3284		Qy 1124 AspCysAı :::    . Db 3404 AACTGTG	Qy 1144 TyrSerGl     Db 3455 AATTCTAC	Qy 1151 SerCysA) :::    Db 3515 AATTGTGC	Qy 1166	1167		Oy 1173 Db 3689 fATGTTGA	Oy 1182A       Db 3749 GATACCAC	Qy 1197 LeuSerLy :::    Db 3809 ATCAGITT	1216	Qy 1236 GluGluTl :::  : Db 3860 GATGCCAC	3908		1296	1316	OY 1336 GIVHISL, Db 4148 AATCATC RESULT 2 US-08-470-350B-1
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7 ValGinGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGlyMetAsnIleAlaGluVal 726 :::III:::     :::    :::	7 ValCysArgGlnLeuGluCysGlySerAlaIleArgValSerArgGluProHisPheThr 746		7 TrpAspCysIleArgTrpGluTrpLysGlnThrAlaCysHisLeuAsnMetGluAlaSer 786   11	LeuileCysSerAlaHisArgGlnProArgLeuValGlyAlaAspWetProCysSer::	GlyargValGluValLysHisAlaAspThrTrpArgSerValCysAspSerAspPheSer	LeuHisAlaAlaAsnValLeuCysArgCluLeuAsnCysGlyAspAlaIleSerLeuSer		846 ValGlyAspHisPheGlyLysGlyAsnGlyLeuThrTrpAlaGluLysPheGlnCysGlu 865 708TCTGGCATCAACAGCA 2725	6 GlySerGluThrHisLeualaLeuCysProIleValGlnHisProGluAspThrCysIle 885 	HisserArgGluValGlyValValCysSerArgTyrThrAspValArgLeuValAsnGly	LysSerGlnCysAspGlyGlnValGluIleAsnValLeuGlyHisTrpGlySerLeuCys :::	ASPThrHisTrpAspProGluAspAlaArgValLeuCysArgGlnLeuSerCysGlyThr 	946 AlaLeuSerThrThrGlyGlyLysTyrIleGlyGluArgSerValArgValTrpGlyHis 965	ArgPheHisCysLeuGlyAsnGluSerLeuLeuAspAsnCysGlnMetThrValLeuGly	986 AlaProProCysIleHisGlyAsnThrValSerValIleCysThrGlySerLeuThrGln 1005 ::: ::: :::	6ProLeuPheProCysLeuAlaAsnValSerAspProTyrLeuSerAlaValPro 1023	4 GluGlySerAlaLeuIleCysLeuGluAspLysArgLeuArgLeuValAspGlyAspSer 1043	4 ArgCysalaGlyArgValGluIleTyrHisAspGlyPheTrpGlyThrIleCysAspAsp 1063
Qy 707 Db 2411	Qy 727 Db 2471	Oy 747 Db 2531	Oy 767 Db 2591		Qy 806 Db 2681		73	Oy 846 Db 2708	Qy 866 Db 2726	Qy 886 Db 2750	~		Oy 946 Db 2885	Qy 966 Db 2945	Qy 986 Db 3005	Oy 1006 Db 3065	Qy 1024 Db 3125	Oy 1044 Db 3164 Oy 1064

1166 1172 3688 1181 3808 3847 1255 1315 1103 3403 ---GluThrGlu 1150 erCysAlaGlyArgLeuGluValPheTyr---AsnGlyThrTrpGlySer----- 1166 ----ArgGlnLeuGlyCysGlyGluAsnGlyValValSerLeu-----AlaPro 1196 suSerLysThrGlySerGlyPheMet---TrpValAspAspIleGlnCysProLysThr 1215 isileSerileTrpGlnCysLeuSerAlaProTrpGluArgArgileSerSerProAla 1235 -----TCCTTCCCAAGC 3859 3907 spLeuAlaGluAlaGluValValCysGlnGlnLeuGlyCysGlySerAlaLeuAlaAla 1295 4027 4087 selyAsnGluSerPheLeuTrpAspCysHisAlaLysProTrpGlyGlnSerAspCys 1335 4147 ATTCTACTACGACAGATTGGTGGCATCCAACAACTACAACCACTGCAAGACCCTCTTCA 3514 STGCATACTACCCCAACAATGCTAAGTGTGTTTGGGAAATAGAAGTGAATTCTGGTTAT 3628 ATGITGAAATCITTGATGGATCATTGAATAGCAGTCTCCTGCTGGGGAAAATCTGTAAT snCysThrGlyThrGluSerHisLeuTrpGlnCysProSerArgGlyTrpGlyGlnHis -----ThrThrAlaIleAlaGlyIleValCys--uGluThrTrpIleThrCysGluAspArgIleArgValArgGlyGlyAspThrGluCys VTGCCACCTTG------AGGTTGGTCAATTTAAATTCATCCTATGT euArgAspAlaSerPheGlyGlnGlyThrGlyThrIleTrpLeuAspAspMetArgCys ------valGlyArgArgAsnIle-------rSerGluThr

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 Lys1leGlnGlyArgTrpGlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaAsp
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Patent No. 5684126
GENERAL INFORMATION:
APPLICANT: Li, Xiao
APPLICANT: Snyder, Solomon H
TITLE OF INVENTION: Ebnerin: A Secreted von Ebner's Gland
TITLE OF INVENTION: Protein Associated with Taste Buds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,350B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-759-130B-381 (1-1453) x US-08-470-350B-1 (1-4360)
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                              33,568
ER: 01107.48790
                                                                                                                       STREET: Banner & Witcoff, Ltd. STREET: 1001 & Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: WOlffe, Susan A
REGISTRATION NUMBER: 33 568
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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41.738
29.588
14.048
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rattus rattus
                                                                                                                                                                                                                                    ZIP: 20001
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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Best Local Similarity:
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : NAME/KEY:
; LOCATION:
US-08-470-350B-1
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338 LeuTrpAspCysArgHisSerGlyThrValAsnPheAspCysLeuHisGlnAsnAspVal 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652 GGCTGTGGGCCTTGTCTGCCCCAGGAAGTGCCCCAGTTTGGACAGGGCTCTGGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 CysSerGlyArgValGluValArgIleHisGluGlnTrpTrpThrIleCysAspGlnAsn
                                                                                                                                                                                                                                                                                                                              398 TrpLysAsnGluGlnAlaLeuValValCysLysGlnLeuGlyCysProPheSerValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 CysThrGlyAsnGluSerAlaLeuTrpAspCysThrTyrAspGlyLysAlaLysArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 LeuValGlyAlaHisSerProCysTyrGlyArgLeuGluValLysTyrGlnGlyGluTrp
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532 CTGGTGAATGGAGGAGAGAGGTCGTGGGGGGTCCTTGGGTTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyThrvalCysHisAspArgTrpSerThrArgAsnAlaAlaValValCysLysGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 IleTrpLeuAspAspValSerCyslleGlyAsnGluSerAsnIleTrpAspCysGluHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832 TCTCAAACAAGCAGTCCCACACCCGATTCTCAAACAAGCAGTCCCACACCCGGTTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    892 AACCCCGGGGGCACAAATAACGATGTGTCCTATGGACCCGAACAGACCACAGACGCAACA
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                                                                                                                                                             -----TCTCAAACAAGCAGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AACCATGGGGGCACAATTAATGATGTGTCTATGAC------ACTCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 CysPheArgArgSerAspAlaGlyValIleCysSerAspLysAlaAspLeuAspLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TTGGCTGTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 GlyCysGlyLysProMetHisValPheGlyMetThrTyrPheLysGluAlaSerGlyPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618 AlaValValCysSerGlnLeuAspCysProSerSerIleIleGlyMetGlyLeuGlyAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                       418 GlySerArgArgAlaLysProSerAsnGluAlaArgAspIleTrpIleAsnSerIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              558 SerGlyTrpGlyLysHisAsnCysValHisArgGluAspValIleValThrCysSer---
                                                        250 CTGTGGAGCTGCTCCCACCGAGGCTGGCTCTCATAACTGTGGACATCAGGAGGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 ---ACAGAAACTTCTCAAACAAGCAGTCCCACACCTGATTGGTGG----
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                                                                                                                                                                                                                                                                                                                                                                                    370 GGCACAAATAACGATGTGATCTACGACACTCAAGAAACC---
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                                                                                                                                             346 ACACCCGGT-
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2132 1152 2692 1216 2058 1003 1016 1034 1074 1094 2414 1114 2593 salaGlyArgLeuGluValPheTyrAsnGlyThrTrpGlySerValGlyArgArgAsnIl 1172 1172 ethrThrAlaIleAlaGlyIleValCysArgGlnLeuGlyCysGlyGluAsnGlyValVa 1192 -----ACATTGAAGTCCCAAACAACTACCGCGTGACTGTGGTCTTCAGAGATGTGCAG 2745 sArgLeuArgLeuValAspClyAspSerArgCysAlaGlyArgValGluIleTyrHisAs 1054 ----CTGAGGCTGGTAAATGGAACAAACCGGTGTGAGGGCCCAGTGGAGATCTTGTACAG 2294 AGGCTCTTGGGTACCGTGTGCCGACGACAGCTGGGACATCAATGATGCCAATGTGGTCTG 2354 sGlnLysLeuGlyCysGlyValAlaPheAsnAlaThrValSerAlaHisPheGlyGluGl ySerGlyProIleTrpLeuAspAspLeuAsnCysThrGlyThrGluSerHisLeuTrpGl :|||:::
cacgaggaggaggggtrccaagcrgactactactccartcaggaccaggacaactcc FGLyPheTrpGLyThrIleCysAspAspGlyTrpAspLeuSerAspAlaHissValValCy Trigorica crocerga receactice - ererecte green erreganda and recentrate 2746 CTGGAAGGGGGCTGCAACTATGACTATATAGAGATTTTTGATGGCCCCCCACCACAGTTCA ----ProCysLeuAlaAsnValSerAs pProTyrLeuSerAlaValProGluGly-----SerAlaLeuIleCysLeuGluAspLy eCysSer----GluPheThrAlaLeuArgLeuTyrSerGluThrGluThrGluSerCy T-----AAACTATACTTGTGGAGGTTTCCTGACTGGAC-TCTCTGGGCAATTTTCTAGC sArgPheHisCysLeuGlyAsnGluSerLeuLeuAspAsnCysGlnMetThrValLeuGl yAlaProProCysIleHisGlyAsnThrValSerVal----IleCysThrGlySerLe sIleSerIleTrpGlnCysLeuSerAlaProTrpGluArgArgIleSerSerPro 1234 LSerLeuAlaProLeuSerLysThrGlySerGlyPheMetTrpValAspAsp----2007 CATCCTGGGTTTTGATGGTCCTGAATACAATTCTTCTCTCATTGCTCGGGTT -----TGTGATGGGTCCAATGGATCTTTCACCTCAACCCAG Domain SRCR

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4010
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4179 CATCCAGATCTCTGGAGGGTTGGGTGGTGGCTCATGCCTTTAATCCCCACACTTTGGG 4238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4239 AGGATGAGGTAGGCAGATTGCTTGAGCTCAGGCGTTCAAGACCAGCTCTAGGCAAGATGG 4298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4359 ITCAGAGAATATAGTAACAGGITICTCACTCCAGGGCCCCCGGCCCAAGICITICCIGGIÍ 4418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4419 ATCTGGTGGCTCTGGAGTTTAGTTGGGGCAGTTGGCCTGTGGGTACAATGCCACGGTCAG 4478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4539 GIGITCAGACACAGGGTCCAGCATGCTGACATCAGAAATGATGAGCTTTTTATTCTGCTC 4598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheAlaMet------PheArgPheGlyGlnAlaValThrArgHisGlyLysIleTrp 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TrpGlySerHisAsnCysTyrHisGlyGluAspValGlyValAsnCysTyrGlyGluAla 151
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                                                                                                                                                                                                                                                                                                35 CysPheLeuIleSerSerPheAsnGlyThrAspLeuGluLeuArgLeuValAsnGlyAsp 54
                                                                                                                                                                                                                                                                                                                                                                                                                          AspGlyTrpAsnThrThrAlaSerThrValValVslysGlnLeuGlyCysProPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuAspAspValSerCysTyrGlyAsnGluSerAlaLeuTrpGluCysGlnHisArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AsnLeuAsnThrAlaAlaValValCysArgGlnLeuGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 AsnLeuGlyLeuArgLeuValAspGlyAsnAsnSerCys----
                                                                                                                                                                                                                                                                     US-09-759-130B-381 (1-1453) x US-09-341-587-6 (1-29598)
                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                           3.89e-61
785.50
26.468
19.328
                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-6
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GlyThr----
                                                  Q ID NO 6
LENGTH: 29598
                                                                                                                                             Alignment Scores:
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Q C		CAGGAACATCGGCATAACTCATACCCCCATTTTCCCCGAGGCTCCTTCTCAGGGACAGCA 4658
Oy	198	CysProSerSerPhe 202
<del>අ</del> .	4659	CGITITGGGGATCTGGTTGGTGAAGCCTTCCCTCCCTTGAACACTGTATTACCTTGAGT 4718
QY	0	
qq	4719	GTTGTCAGCCGCTGACCCAGAGGGAAGGATGCAATTGTAAATAGTTCACTTATGATTGCT 4778
QY	215	ArgProlleTrpLeuAspAsp1leLeuCysGlr
qq	4779	GTGAAGAGAGGCAGGGAAGTGGGGTAAGGGTGGGAGGATGGCAGT 4823
δλ	228	GluLeuAlaLeu-TrpAsnCysArgHiSArgGlyTrpGlyAsnHiSAspCy 244
οg	4824	
Qy	244	
qq	4884	GIATCACCAGGAATCCACGTCAAACCTCAGACTCATCGCAGCTCAAGCGTGGAGAGTTAG 4943
Qy	250	ValThrLeuThrCysTyr
qq	4944	
QY	261	
qq	5004	_
Qy	267	-GlyThrAsnArgCysMet272
qq	5064	AGGCACAGAGAGGCAATGCCAGGGGCTGTGGGGTCCCTGAGGGACCGAGGGGTTCACGG 5123
Oy	273	
qa	5124	TGGGCACTGGCAGGGCCCACTTGGTGGGCGTGTGGGCATCAGCTCAGGGTGTAGATA 5183
Qγ	281	281
qq	5184	CCCCAAGTCACTTCAGCCTTAACTCTACTTGGAGTCACTGAGTGTTTGGTGTCTAATGTT 5243
Qy	281	281
qq	5244	GCTATITITITICTCACAGCTGCCCAGCCTCAGTCAACACTCAGGCCAGGTGAGTCCCCCAG 5303
ΟŊ	281	281
qq	5304	AAICCITCCICGGGAIACCCCTICITTTCIGCICAGITACCCCIICCCIACICCACAGA 5363
Qy	282	lyThrv
qq	5364	GCCCTCCTGCTTCTCTGCAGATACTCTGGGGCATATTATTTCACCCCCAACTCTGTAACT 5423
QΣ	289	296
QO.	5424	GAGACCCTAGCATGGGGCTTCTTAACCACACATGGGATTTAGCTTCTGCCTTCTTCAG 5483
Qy	297	
QQ	5484	
Qy	301	!
qq	5544	AGAAAGAAGCCTGCTGTTTAATGAGCTTTGGCCTGTTATATTCAGGGCTGACACCT 5603
οy	314	314
qq	5604	TTCTGGGAATTGAGGGTGAGACTCTCTAATGTTCTGTTGAAGGCAAGGTCAGTACAGGCT 5663
QY	315	317
QQ	.5664	TGATACCCCCATCTCACTACTTGAAAAACCCCCAGATTCTGCAGGGCCACGTCTGCAT 5723

13.7   13.7			•
TCAGAAGAGGCAGAGGCCATGCTGAGGGAGAGAGCTAAGAAATGTTTCTGGTGGCT TCACTTACCAGGGCAAAACCTGATTTCCCCCAGGGCGGACCCTAGTATTCCCGAACTTTTTCCTAGTACCAGGGCGAACGCTCTCTCCGAAGGAACCTCTCTCT	317		17
TCACTTACCAGGAAACCTGATTTCCCCCAGGCGGGCCCCTAGTATCCGGAACATTTTAG  CTGCAAGTGCAAGTCTTGCTACTTCTACTGGAATGGCCAGTCAGT	5724	TCAGAAGAGGCAGAGGCCATGCTGAGGGGAGAGAGAGGGCTAAGAAATGTTTCTGGTGCCT	783
TCACTTACCAGGAAACCTGATTTCCCCCAGGGCGGACCCCTAGTATCCCGAACATTTTAG	317		17
CTGCAAGTGCAAGTGCTGCAATGACCAATGACCAGTCAGT	5784	TCACTTACCAGGAAACCTGATTTCCCCCAGGGGGGGGACCCCTAGTATCCCGAACATTTAG	843
CTGCAAGTGTCAAGTCTTGGCAGTGTGTCAAGTGGCAATGGTCCACGGCGTCAGTGG  AGGGGGGGTGGTGAAGGTTTCCTAACTGCGAATGGTCACTCCTCTCAG  AGAGAGTGGAAGGGCTGCATGGTCCTTTGTCCCTGAATGAGTTCCTTCTCAG  AGAGAGTGGAACACATGGGCAACAGTGCCTTTGTCCCTGAATGAGTTCCTTTTCAC  SETGLYThtValAsnPheAsppysbuth 4501 hasnAspval	318	GlnSerGlySerAspVal	23
AGGGGGGAGGGGGGGGGGGGGGGGGGGAGGGGGGGGGG	5844	CTGCAAGTGTCAAGTCTTGGCAGTGGTGTCAGATGAGCCAGTCAGT	903
AGGGGGGGGGGGGGGGGGGGGGGGGGGAATGCCTCTCTCGGGGAGGGGGGGG	323		23
AGAGAGGGGCCTGCATGGTGTCCTTTGTCCCTGAATGAGTTCCTGGGCAGGAG ValtrpleuAspGlyValSerCysSerGlyAsnGluSerPheLeuTrpAspCysArgHis	5904	ATGGTGGGGGATGGGGGTGGTGAAGGTTTCCTAACTGCGAATAGGTCATCCCTCTCAG	963
AGAGAGGTGGAAGGCCCTGCATGGTGTCCTTGTCCCTGAATGAGTTCCTTGGGCAGGAG ValTrpLeuAspGlyValSerCysSerClyAsnGluSerPheLeuTrpAspCysTglis	323		23
ValIrpleudapGlyValSerClyAsnGluSerPheleuTrpAspCysArgHis	5964	AGAGAGGTGGAAGGGCCTGCATGGTCCTTTGTCCCTGAATGAGTTCCCTGGGCAGGAG	023
ACCTGGGCAGACACATGGGGAAGTGGCCAGACCTTCGAGTGGAATTGTTTTCAC SerClyThrvalasnPheAspCysLeuHisGlnAsnAspVal	324	ValTrpLeuAspGlyValSerCysSerGlyAsnGluSerPheLeuTrpAspCysArgHis	43
SerGlyThrValAsnPheAspCysLeuHisGlnAsnAspVal	6024	ACCTGGGCAGACACATGGGGAGCAAGTGGCCAGACCTTCGAGTGGAATTGTTTTCAC	080
CTTCAAGTCCAATTGTACCTTTTGTTGCTGTTTACAGAAAGTTG-GCCTGTCAG  ASP	344 6081	SerGlyThrValAsnPheAspCysLeuHisGlnAsnAspVal	57 125
CTTCAAGTCCAATTGTACCTTTGTTGTTGTTGTTTACAGAAAGTTG-GCTGTCAG  ASP	358	SerVallleCysSer	62
ASP	6126		184
TTCTACCTCTGGATACACTTTGGATTTCATAGTTCACTTATGATTGCCATAAAGAGGGGGGGAGGGA	363 6185	ASPGlyAlaAsp	56
TTTCTACCTCTGGATACACTTTGGATTTCATAGTTCACTTATGATTGCCATAAAGAGAGG  TGGGGAAGTGGCTAAGCGTGGAGGTGGCAGCTGGATAAACAGTTGCCTCAAGAGT  ArgleualaspGlySearGAAGAGGGGGGGGGGGGTGGATAAACAGTTGGCTCAAGAGT  ***I	366		99
TGGGGAAGTGGCTAAGCGTGGAGGGTGGCAGCAGGTGATAAACAGTTGGCTCAAGAGT  ArgLeuAlaAspG1ySerAsnAsnCysSerG1yArgValG1uValArg1leH1s  :::	6245	TTTCTACCTCTGGATACACTTTGGATTTCATAGTTCACTTATGATTGCCATAAAGAGAGG	304
TGGGGAAGTGGCTAAGCGTGGAGGTGGCAGCTGATAAACAGTTGGCTCAAGAGT  Arg LeualaaspGlyasaAsnAsnCysSerGlyargValGluValArgIleHis  :::	367	renglnFen	. 69
ArgleualaapGlySerasnasnCysSerGlyArgValGluValargIleHis :::   :::    :::    :::    :::    :::       :::       ::        ::	6305	TGGGGAAGTGGGCTAAGCGTGGGAGGCTGGCAGCAGGTGATAAACAGTTGGCTCAAGAGT	364
CATGATAGGATCAGGTCGGCCCCTTGCTTTTCATGTTTCTGTGGGTTGGTA	376	ArgLeuAlaAspGlySerAsnAsnCysSerGlyArgValGluValArgIleHis :::       :::	87 424
CATGATAGGATGAGGTCAAGGTGGGCCCCTTGCTTTTTCATGTTCTGTGGGTTGGGTA	387		87
GGGAGGAAGCTGCAAAACCCAGAATTAGATGTGATATTGGAGGGTGGAGGT	6425	CATGATAGGATGAGGCTCAAGGTGGGCCCCTTGCTTTTTCATGTTTCTGTGGGTA	484
GGGAGGAAGCTGGAGTCTCTGAAAACCCAGAATTAGATGTGATATTGGAGGGTGGAGGGT	386	GluGlnG	
GCTGGTGACCTGTCTGGGGATCCTGTTCCAAGTGGTCAAAAAGATCCTTATC  TATGGCTCAGAACAACCCTGGGGTCTCCCTAATCCTATGGGGACCTCATCCTGCCA  TCTCTGGTACTCTGCCAGTCCCAGATAGGACCATGCTCCTGCCA  TCTCTGGTACTCTGCCAGTCAATAGGACCATGCTCTGCGGGGTTCTCTGGGGAGGGGTTCTCTGGTAATAAGGGAGGG	6485		544
GCTGGTGACCTGTCCTGTGGGATCCTGTTCCAAGTGTCCAGAAAAGATCCTTATC  TATGGGCTCAGAACAAGCCCTGGGGGTCTCCCTAATCCTATGGGGACCTCATCCCTGCCA  TCTCTGGTACTCTGCCAGTCCCAGATAGGACCATGCTCCTGAATAAGGGAGGG	394	CysAspClnAsnTrpLysAsn	. 00
TATGGGCTCAGAACCCTGGGGGTCTCCCTAATCCTATGGGGACCTCATCCTGCCA  TCTCTGGTACTCTGCCAGTCAGATAGGACCATGCTCCTGAATAAGGGGGGGT  CTCTGGTACTCTGCCAGTCAGATAGGACCATGCTCCTGAATAAGGGAGGG	6545	GCTGGTGACCTGTCCTGTGGGATCCTGTTCCAGAGTGGTCAGAAAGATCCTTATC	601
TATGGGCTCAGAACCCTGGGGGTCTCCCTAATCCTATGGGACCTCATCCCTGCCA TCTCTGGTACTCTGCCAGTCAGAATAGGACCATCTCTGAATAAGGGGGGT TCTCTGGTACTCTGCCAGTCAGAATAAGAACTCAATCAGGAATAAGGGGGGGT TCTCTGGTAACTCAGCAACTCAATCAACAACAACAACAACAAAAAAAA	400		00
TCTCTGGTACTCTGCCAGTCAGATAGGACCATGCTCCTGAATAAGGGAGGG	6602	TATGGGCTCAGAACAAGCCCTGGGGGTCTCCCTAATCCTATGGGGACCTCATCCCTGCCA	661
TCTCTGGTACTCTGCCAGTCAGATAGGACCATGCTCCTGAATAAGGGGGGTGluGlnAlaLeuValValCysLysGlnLeuGly	400		00
GluGlnAlaLeuValValCysLysGlnLeuGly	9999	TCTCTGGTACTCTGCCAGTCAGATCCCAGATAGGACCATGCTCCTGAATAAGGGAGGG	721
	401	GluGlnAlaLeuValValCysLysGlnLeuGly	11

Qy Dp	412Cysprophese	SerValPheGlySerArgArgAlaLysProSerAsnGluAlaArg 4: :::             ACATCCACTGGGGTCACAGGTGCTTCCCCAAAAGTTGAGCATCCA 6	429 6841
δλ	430 AspileTrp	lleAsnSerIleSerCysThrGlyAsnGluSerAlaLeuTrp 4	46
qq	 2 TAGACCTGGGCAGAGT	:::      ::	
ογ	spCysThrTyrAspG	yLysAlaLysArgThrCys	458
qq	L	ATATECAAAGGTGACTGCCTGCCTAGGTGACTTAGTTCATTAG 6	6946
Qy			64
qq	6947 GAAGTACCCTGAGTGT	GAACTTACCTTAGATTCTTGACCTCATGA	9007
Qy	GlyvalileCysSer-	AspLysAlaAspLeuAspLeuArgLeuValGlyAla 4	81
qq	7 GGGTTCT	GGATCTGAATCCAGTTTGGCCCTGAGGCTGGTGAATGGA 7	9902
ΟŸ	Pr.P	roCysTyrGlyArgLeuGluValLysTyrGlnGlyGluTrpGlyThrValCys 5	0
qq	7067 GGCGACAGGTGTCGAG	7	7126
Qy		HisaspargTrpSerThrargasnalaalavalValCysLysGlnLeuGlyCysGlyLys 5	21
qq	7127 GATGACTACTGGGACA	CCAATGATGCCAATGTGGTCTGCAGGCAGCTGGGCTGTGGCTGG 7	7186
οy	522 ProMetHisValPheG	.isValPheGlyMetThrTyrPheLysGluAlaSerGlyProIleTrpLeuAsp 5	541
qq	7187 GCCATGTCAGCCCCAG	7	7246
Qy	542 AspValSerCysIleG	YrrpGly	561
අ <u>ධ</u> :	7247 GATGTGCGCTGCTCAG	TGTGCGCTGCTCAGGACACGAGTCCTACCTGTGGAGCTGCCCCCACAATGGCTGGC	7306
Οy	562 LysHisAsnCysValH	AspAla 5	579
QQ	7307 ACCCACAACTGTGGCC	TTCAAGA	7366
Οy	580 ThrTrpGlyLeuArgL		595
QQ	7367 ACTIGGCTCACTCTC	rigg-ggrggagtrrgcrccaaagaaactcctaatta 7	7419
Qγ	296	uValTyrPheGlnGlyArgTrpGlyThr	909
Dβ	7420 CATTCTGATCTCCTCACT	CAAAGCTTCTATGTTTTCTATGTTTCTGAAGACTTGTCAG	7479
Οy	607 ValCysAspAspGly	TrypAsnTrpAsn	613
QQ	7480 CÉCTGCTAGAATCCA	PATGTACTCACTGCCTAGTGTTCCTGTGGTCACTTAGGACAGGG 7	7539
Qy	614	_	620
q	7540 GATCAAACTAAAACAA	GATCAAACTAAAACAACCCAGAGTTTTTCCCCTTCCTGAGGCAAGGCAAGGAAGAGGCAG 7	7599
Qy	621 CysSerGlnLeuAspC	_	640
QQ	7600 AAGAGAAAAGTGCCGG	TILL STATE S	7659
Øγ	641 GlyTyrGlyLysileT		655
QQ	7660 GGTATAATGGATGCA	SCAAGGCAGGGATCCCTCACTGCGAGGAA	7719
Oy	929	-	629
qq	7720 CTCTGAACTAAAGATG	AGTGGGTTCTCAGCTGAGACCCAGTGAGGTC 7	6777
Qy	gAsn	yTrp	299
Op	SAAATAGAGGCTC	TTAGGAGTGCAAATGGGTGTCTGTTTGTATCAGGCCTGGG	7839
δŏ	668GlyA	lyAsnAsnAspCysSerHisSerGluAspValGlyValIle 6	681

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7840 TIGCGIGGGGITGGAGTICITGACCICAGCICTICICAGAACGCIGGGGGTIGCCTG	b82 CysSerAspAlaSerAspMetGluLeuArgLeuValGlyGlySerSerArgCysAlaGly 701          ::: :::	702 LysValGluValasnValGlnGlyAlaValGlyIleLeuCysAlaAsnGlyTrpGlyMet 721 11111111111111111111111111111111111	722 AsnIleAlaGluValValCysArgGlnLeuGluCysGlySerAla 736	737 IleArgValSerArgGlu	751HisileLeuMetSerAsnSerGly	762 yGlualaSerLeuTrpAspCysIleArgTrpGluTrpLysGlnThralaCysHisLeuAs 782	782 nMetGluAlaSe 786	8209 CTAGGATGGACTGAGTGTCAGACTCGCTCATTTCTTTCCCTCCTCGTTCCAGTTTTGCCG 8	786 rLeuIleCysSer 790           8269 ACTICIGIGIAAIGIICCIGAICIGACCIICTCIITCICACAGCICCCCAGICCC 8328	791 -AlaHisArgGinProArgLeuValGlyAlaAspMetPro	803 803	8389 TGCCCAATCACCCCTTCCACACTCCACAGAGCTCTCTTTTCTCTGTGTGGATACTGTG 8448	803 803	8449 GGGCATATTATTTCCACCCCAACACGGCTGTGTAACTGAGATCCCAGCACAGGGCTTT 8508	803 803	8509 ITAAACACACACAGGAITGAGGAGGCCTCTGTCTTTTCAACCCCTCTCAGCTTTCAI 8568	803	8569 GAAACAGITICATACIGICCCAGIGGACAACCCITACAGGITCAGGAAGIGGCCCCAIGI 8628	803 803	8629 ITAATGAGCTTTGGTCCTTTTATATTCCGGACTCACATATAGTTTCTGAAAATTGAGGGT.8688	804	8689 GTCACCCTCTGACCCGTTCAAGGCATCGT	813 -AlaAspThrTrpArgSerValCysAspSerAspPheSerLeuHisAlaAlaAsnValLe	8749	832 uCysArgGluLeuAsnCysGlyAspAlaIleSerLeu	844 844
qq	do Db	QY Db	9 9	ç d	δ P	Qy Db	οy	Q	Oy Op	Qy Db	٥y	Ω	δy	qq	δy	qq	Οy	qq	Qγ	qq	ογ	qq	0y	g	Q D	οy

6366	9900 TGCAGCCATCTGCCATTGTGACTGCGTGCCCTGGTGACTTTGGCATTTGTATTCAAACTT	g
1016	1016	Óγ
6686		qq
1016		ò
1004 9839	992GlyAsnThrValSerVallleCysThrGlySerLeuThr	QQ
6176	9735 TGTAGCTGTGTAGCTCCATCCTGTGTTCACCCAGAGTGGGGAGTG	QQ
991	977 AspAsnCysGlnMetThrValLeuGlyAlaProProCysIleHis	ΟŊ
9734	9693 CCAATAAGCTCCTGAATATGGAGGGGGTCTAGGCCTGTCATT	Op
916	SlyHisArgPheHisCys	QΥ
962	943 ysGlyThrAlaLeuSerThrThrGlyGlyLysTyrIleGly-GluArgSerValArgVal 	ΟY
9632	9573 CTCAGGCCATGGGATCCAGACCTCTGAAGAGCGGGTGAAAGTGCCGGTCCCTGCACCTGT	о́р
943	931 roGluAspAlaArgValLeuCysArgGlnLeuSerC	Οy
9572	9516 GIGCICAGGACGAGCACTGGAGGCTCCTTAATGCTGGGACCTCATTCCTGGCC	d d
9515	iggicaggaagaiccicaic	qq
922	920HisTrpG	Qy
9455	•	: A
0.00	9330 AMACIGAINGGAIGAGGCICANIGIGGGCIICICAITICANIGICCCIGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3
0	898ThrAspValArgLeuValAsnGlyLysSer	δŽ
9335	ACCCTCTCACCCTCCCTAGGACTCACTATCTCTGGAC	qq
897	888 rgGluValGlyValValCysSerArgTyr	Qy
92	TCTTTTCCTTTGTTGCAATTTACAGATACTTGGCCG	qq
176	30 CGIIGHIICCICCCAGAGAICCIIIIGIICIGIGCCIIIIICCCCIICAGAGAICCIIII	2
882	875 rolleValGlnHisProGluAsp	0 Y
9155	9096 GGAGACCTGGGAAGACAAATGGCAAGAACAAGAAGAAGAAGAAGAAGTGGAATTGTTGTCA	qq
875	857ThrTrpAlaGluLysPheGlnCysGluGlySerGluThrHisLeuAlaLeuCys-P	Qγ
3606	9036 AATGGAGGGCTCAGTCTGGTCTCCAGGAGCCTTTGTCCCTGGATGAGTTCACAGCACA	qq
856	856	δy
9035	111 111:: 8985 GCATGGTGGGGGCATCCTCTAACAGATAGAAAGATACCCCAGGATTACAGA	Dp
856	heGlyLys	Qy
8984	8925 CGAGCTTCAGCAATGGCGTCTGATGTCCTAGTCAGTCCATGCATCAGCAGATGTGGGATG	Db
848	45SerValGl	Qy
8924	8865 IGATICCIGATIGICCCCTGGGCAGCCCCTGGIICCCCTAACAITITACCIGGCAGIGIC	g

euargaspalase 1300 ||:::||| ||GaaaGar---- 11109 erSerGlyHisLe 1360 :: CCCAGAACCACAG 11189 1yCys----- 1289 ||||||| |GATGTGACAAGCC 11054 ----- 11133 ysGlyAsnGluSe 1320 oCysLeuAlaAsn 1013 eCysLeuGluAsp 1033 TACTTGGCTGACC 138 sGlyAsnThrVal 995 CATGAAGATGCT 78

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TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR
TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND MONOCLONAL
TITLE OF INVENTION: ANTIBODIES THERETO
1326 HisalaLysProTrpGlyGlnSerAspCysGlyHisLysGluAspAlaGlyValArgCys 1345
                                        1162 CGGAACCGAGGCTGGTTCTCCCACAACTGTAATCATCGTGAAGATGCTGGTGTCATCTGC 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --TTGATCCTTGCCATTTGCACCAGACCTGGATTC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuileSerSerPheAsnGlyThrAspLeuGluLeuArgLeuValAsnGlyAspGlyPro
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148
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139
31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                3: ROBINS & ASSOCIATES
90 MIDDLEFIELD ROAD, SUITE 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,956
FILING DATE: 06-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/034,916
FILING DATE: 04-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   Sequence 1, Application US/09034916
Patent No. 6046314
GENERAL INFORMATION:
APPLICANT: GEBE, JOHN A.
APPLICANT: STADAK, ANTHONY W.
APPLICANT: ARUFFO, ALEJANDRO A.
                                                                                                                       1222 TCAGGAAACCATCTATCGACA 1242
                                                                                SerGlyGlnSerLeuLysSer 1352
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (650) 325-7823
FORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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STATE: CATTLE
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Query Match:
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US-09-034-916-1
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                                                                   TrpAsnThrThrAlaSerThrValValCysLysGlnLeuGlyCysProPheSerPheAla 96
                                                                                                                                                                                                                            148 TyrGlyGluAlaAsnLeuGlyLeuArgLeuValAspGlyAsnAsnSerCysSerGlyArg
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                             ThralaalaValValCysArgGlnLeuGlyCysProSerSerPhelleSerSerGlyVal
                                                                                                                                                                    TCAGTCAGTTGCACAGGAACAGATACATTGGCTCAGTGTGAGCAAGAA-----
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Patent No. 6140056
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
  ||| |||| CTAGCGTCTCCATCTGGA----
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TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES ITITLE OF INVENTION: USES THEREFOR FILE REFERENCE: NUI. 0/3 CURRENT APPLICATION NUMBER: US/09/276,400 CURRENT FILING DATE: 1999-03-25 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3
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Gaps:
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Query Match:
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TYPE: DNA
ORGANISM: HOMO S
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	QY	684 2003	sp-alaseraspMetGluLeuargLeuValGlyGlySerSerarg    :::::          ::          arctalceGGCargacattGaCTGTCAGTGGATTGACATCACGG	1LeuArgLeuVal      \TTGACTGTCAGT	Glyglyserserar       GGATTGACATCACG	9 698  -   2047	
	RESULT US-09- 1 Pacted 1 Pacted 1 APP 1 TILL 1 CUR 1 CUR	SULT 7 SUCT 7 SOG-448-076 Sequence 3, GENERAL INF APLICANT: TITLE COURENT AP CURRENT AP CURRENT AP CURRENT AP EARLIER FI EARLIER FI EARLIER FI EARLIER FI EARLIER FI LONGHES SOGTWARE: SEQ ID NO 3 TYPE: DNA TYPE: DNA CRGANISM:	76-3 3, Application 6300092 NECRMATION: T: Khodadoust, TINENTION: MET BERNCE: MNI-073 APPLICATION NUM APPLICATION NUM FILING DATE: 19 FILING DATE: 10 FILING D	US/09448076 Wehran et al. HODS OF USE OF 1CP CP EP (SP) 99-11-23 BER: 60/117,580 BER: 60/117,580 BER: 09/276,400 99-03-25	A NOVEL LYSYL ,,076 10	OXIDASE-RELATED	PROTEIN
	Alignmen Pred. No Score: Percent & Best Loc Query Ma	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	t Scores: 6.12e-4 5.1. 6.12e-4 Similarity: 40.038 al Similarity: 27.5438 tch: 4	<u>ه</u>	Length: Matches: Conservative: Mismatches: Indels: Gaps:	2262 214 97 253 32	
	60-sn	-759	-130B-381 (1-1453)	x US-09-448-076	076-3 (1-2262)		
	Qy	30	LeuLeuLeuAsnSe              CTGCTGCTG	SPheLeulleSer	SerPheAsnGlyTh       TCGTGCTTGGGGTC	rcysPheLeuIleSerSerPheAsnGlyThr	44
	Qy	45	GGCCCTGAGAAGAAGGCCGGGAGCCAGGGCTTCGGTTCCGCTGGCTTCCCCAGG	Asp	LeuGluLeuArgLe       CTTCGGTTCCGGCT	-AspLeuGluLeuArgLeuValAsnGlyAsp 	54 153

	75	8 rva	0v 35
	358	8 uTrpAspCysArgHisSerGlyThrValAsnPheAspCysLeuHisGlnAsnAspValSe	33 33 00 114
	1148		1
	338	8 nSerGlySerAspValValTrpLeuAspGlyValSerCysSerGlyAsnGluSerPheL	3y 31
	318 1088	<b>&amp; o</b>	2y 29 Ob 102
	0	9 GAAGGCCAGCACATGGGGCCACA	6
	298	8 slleGlnGlyArgTrpGlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaApV	72 YC
	, iii	99 6	6
	278	σ	2y 25
	0	:::    9 AGGCCTGTCTACGCGCATCCAGTGGCCAGAAGAAGCA	σ.
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	239	9 uAspAspIleLeuCysGlnGlyAsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTr :::	0y 21
	728	0 AGGGTCAACGC-GGCCTTCTACAGGCT	C9 q0
	219	2 PhelleSerSerGlyValValAsnSerProAlaValLeuArgProlleTrp	2y 20
	201	3 GlytrpasnLeuasnThralaalaValValCysargGlnLeuGlyCysProSerSer	2y 18 ob 61
•	781	<pre>3 Sercysserctyargvalciuvallysrmecincludigitpolyinflecysaspasp</pre>	Jy 10
	549	6	3b 49
	162		2y 15
	498	9 CAGCGCCTCCCTGGCTTCTCGGACTCCAATGTCATTGAGGTAGAGCATCACCT	3b 43
	153		3y 14
	147	O ArgGluTrpGlySerHisAsnCysTyrHisGlyGluAspValGlyValAsnCy:	2y 13 37
	378		31 31
	129	0	3y 11
	109 318	5 Pheala	2y 9 3b 26
	94	snThr	2y 7
	74 213	5 GlyProCysSerGlyThrValGluValLysPheGlnGlyGlnTrpGlyThrValCysAsp	2y 5 3b 15

qq	1209	GETCCGGTGCAACCTACCTTACACTGGGGCAGAGACCAGGATCCGACTCAGTGGGGGCCG 1268
ογ	375	rAsnAsnCysSerGlyArgValGluValArgIleHisGluGlnTrpTr 391 :::
qq	1269	၁၁၁၅
οy	391	PThrIleCysAspGlnAsnTrpLysAsnGluGlnAlaLeuValValValCysLysGlnLeuGl 411
qq	1329	CCTCATCTGTGGGGATGACTGGGGGACCCTGGAGGCCATGGTGGCCCTGTAGGCAACTGGG 1388
οy	-	r 429
gg	1389	14
Qy	429	
qq	1449	AGAGGTGGTGATGAGTGCGCTGCACAGGGACTGAGCTGTCCCTGGATCAGTGTGC 1508
δy	449	rTyraspGlyLysalaLysArgThrCysPheArgargSerAspAlaGlyVa 466
qq	1509	CCATCATGGCACCCACATCACCTGCAAGAGGACAGGGACCCGCTTCACTGCTGGAGT 1565
δ δ	46	986
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qq	1631	CCGGCCCCTGCATATGTTGTACTGTGCTGCGGAAGAGAAC
οy	CI	
qq	1679	rggccagctcagcccgctcagccaactggccctatggtcaccggcgtctgctccga
Οy	538	eTrpLeuAspAspVal-SerCys
qq	1739	CTCCCAGATCCACAACCTGGGACGAGCTGACTTCAGGCCCAAGGCTGGGCGCCAC
δy	550	rAsnIleTrpAspCysGluHisSerGlyTrpGlyLysHisAsnCysV
QQ	1799	
δ	569	spvalilevalThrCysSer
QQ	1838	TTCACTCACTATGATATCCTCACCCCAAATGG
Qy	584	rgLeuValGlyGlySerAsnArgCysSerGlyArgLeuGluValTyrPheGlnGlyArgT 604
qq	1888	AGGG
Οy	604	rpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaValValCysSerGlnL 624
QQ	1901	AAGCTAGTTTCTGT 1914
٥y	624	oSerSerIleI
Op	1914	1914
οy	644	IleTrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCysAr
QQ	1915	CGAAGACACTGAGTGTCAGGAGGATGTCTCCAAGGGGTATGAGTGTGCC
δy	664	snSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAspValGlyValIleCysSerA 684
Ор	1961	TTTGGAGAG(
δλ	684	sp-AlaSerAspMetGluLeuArgLeuValGlyGlySerSerArg 698    ::::::             :::     :::

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                                                                                                       TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: USES THEREFOR FILE REFERENCE: MNI-073
CURRENT APPLICATION NUMBER: US/09/702,572
CURRENT FILING DATE: 2000-10-31
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2262
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2003 ATCTCTACCGGCATGACATTGACTGTCAGTGGATTGACATCACGG 2047
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                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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                                                     Sequence 3, Application US/09702572 Patent No. 6391602
                                                                                  GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
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634.50
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; ORGANISM: Homo sapiens
US-09-702-572-3
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Best Local Similarity:
Query Match:
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                                                                                                                            GCATGGGGTGGCGTGCGTGGGCACGGAGGCCCACCTCTCCTTCTTGTTCCTA
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  183 GlyTrpAsnLeuAsnThrAlaAlaValValCysArgGlnLeuGlyCysProSer---Ser
                                              GGCTGGAGCGCCCACAACAGCCACGTGGTCTGCGGGATGCTGGGCTTCCCCAGCGAAAAG
                                                                                             202 PhelleSerSerGlyValValAsn-----SerProAlaValLeuArgProIleTrp-Le
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:::         :::    	TyrPheLysGluAlaSerGlyProll 538	eTrpLeuAspAspVal-SerCys	AspCysGluHisSerGlyTrpGlyLysHisAsnCysValHisArgG 569 :::        GAGTGCCATGGGCATTACCACAGGA 1837	IUASPVal	rgLeuValGlyGlySerAsnArgCysSerGlyArgLeuGluValTyrPheGlnGlyArgT 604 :::	rpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaValValCysSerGlnL 624	AAGCTAGTTTCTGT1914 euAspCysProSerSerIleIleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyrGlyL 644		ysileTrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCysArgA 664	SnSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAspValGlyValIleCysSerA 684	698 2047		5400	18 DEWTETN AND NITTED ACTO MOTEOTIES AND		709/276,400 5						Length: 2920 Matches: 214	tive:	Indels: 215 Gaps: 32	
			erAsnileTrp    :::     CTGGGTGTGGCAC	luAspVal					ysileTr			5-400-1	Sequence 1, Application US/09276400 Patent No. 6140056 CENEDAL INFORMATION.	ENERAL INFORMATION: APPLICANT: Khodadoust, Mehran THTE OF INVENTION: NOVEL, MED-18	TITLE OF INVENTION: USES THEREFOR MAILE REFERENCE: MAIL-073	CURRENT APPLICATION NUMBER: US/09/276,400 CURRENT FILING DATE: 1999-03-25	RE: Patentin Ver. 2.0	SEQ ID NO 1 LENGTH: 2920		'KEY: CDS    ION: (143)(2401) 	•		nilarity: Similarity:		
Db 1631		Qy 538 Db 1739	Qy 550 Db 1799	Qy 569 Db 1838	Qy 584 Db 1888	Qy 604	Db 1901 Qy 624	Db 1914	Qy 644 Db 1915	Oy 664 Db 1967	Qy 684 Db 2003	RESULT 9 US-09-276-400-1	; Sequence; Patent	APPLIC TITLE	TITLE	CURREN	; NUMBER ; SOFTWA	; SEQ ID NO 1 ; LENGTH: 2	CRGANISM: FEATURE:	; NAME/KEY: ; LOCATION:	1.2-60-60	Pred. No.: Score:	# 3	We.	

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163 SercysSerGlyArgValGluValLysPheGlnGlùArgTrpGlyThrIleCysAspAsp 182 | 182 | 183 | 184 | 185 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 187 | 1
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                                                                                                     95 PheAla-------MetPheArgPheGlyGlnAlaValThrArgHisGlyLys 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 GAGGCCACAGGCTGGACCCACAGTGCCCAAATATGGCCCTGGAACA------GGCCGC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 IleTrpLeuAspAspValSerCysTyrGlyAsnGluSerAlaLeuTrpGluCysGlnHis 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 PhelleSerSerGlyValValAsn-----SerProAlaValLeuArgProIleTrp-Le 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           871 GCATGGGGTGGCGTGGGCACGGAGGCCCACCTCTCCCTCTTCCCTGGAGTTCTA 930
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931 TGTGCCAATGACACCCCCAGGTGCCCTGGGGGGCCCTGCAGTGGTGAGCTGTGTGCC 990
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                                                                                                                                                                                                                                                                                                          54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 AspGlyTrpAsnThrAlaSerThrValValCysLysGlnLeuGlyCysProPheSer 94
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09-759-130B-381 (1-1453) x US-09-276-400-1 (1-2920)
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APERRAL INCORDATION:
APPLICANT: Khodadoust, Mehran et al.
APPLICANT: Khodadoust, Mehran et al.
TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
TITLE REPERENCE: MNI-073CP
URRENT APPLICATION NUMBER: 105/09/448,076
URRENT APPLICATION NUMBER: 60/11/380
ARRIER FILING DATE: 1999-01-27
BARLIER APPLICATION NUMBER: 09/276,400
BARLIER FILING DATE: 1999-03-25
SARLIER FILING DATE: 1999-03-25
WUMBER: OF SEQ ID NOS: 122
                                                                                       2057 -----CTCGAAGACACTGAGTGTCAGGAGGATGTCTCCAAGCGGTATGAGTGTGCCA 2108
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644.yslleTrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCysArgA 664
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LOCATION: (143)..(2401)
9-448-076-1
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ORGANISM: Homo sapiens
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g	521	CGGGGCTGGGGGAACAGTGACTGTACGCACGATGAGGATGCTGGGGGTCATCTGCAAAGAC	280
٥y	148	TyrGlyGluAlaAsnLeuTyrGlyGluAlaAsnLeu	153
q	581	CAGCGCCTCCCTGGCTTCTCGGACTCCAATGTGAGGTAGAGCATCACCTGCAAGTG	640
ογ	154	GlyLeuArgLeuValAspGlyAsnAsn	162
qq	641	GAGGAGGTGCGAATTCGACCCGCCGTTGGGTGGGGCAGACGACCCCTGCCC	1691
ογ	163	SerCysSerGlyArgValGluValLysPheGlnGluArgTrpGlyThr1leCysAspAsp	182
qq	692		751
δ'n	183	GlyTrpAsnLeuAsnThrAlaAlaValValVysArgGlnLeuGlyCysProSerSer	201
q	752		811
δò	202	PhelleSerSerGlyValValAsnSerProAlaValLeuArgProlleTrp-Le ::::::     :	219
q	812		870
δy	219		
QQ	871		930
oy .	239	pGlyAsnHisAspCysSerHisAsnGluAspValThrLeuThrCys	254
QQ	931		066
ογ	255		258
QQ	991	AGGCCCTGTCTACGCGGCCATGCCAGAAGAAGCAACAACAACAGTCGAAGCCTCAGGG	1050
ý	259		278
ор	1051	GAAGGCCCGTGTCCGTCTAAAGGCGCGCCCCTGGAGAGGCCGGGTAGAAGTCCT	1110
οy	278		298
QQ	1111	GAAGGCCAGCACACACACACACACGCAAGTGGGACCTGCATGCA	1170
οy	298	1ValCysLysGlnLeuGlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGl	318
qq	1171		1230
ογ	318	nSerGlySerAspValValTrpLeuAspGlyValSerCysSerGlyAsnGluSerPheLe	338
a	1231		
Qy	338	uTrpAspCysArgHisSerGlyThrValAsnPheAspCysLeuHisGlnAsnAspValSe	358
a D	1291		1350
δλ	358	rVallleCysSerAspGlyAlaAspLeuGluLeuArgLeuAlaAspGlySe	375
QQ	1351		1410
ογ	375	rAsnAsnCysSerGlyArgValGluValArgIleHisGluGlnTrpTr	391
qq	1411		1470
ολ	391	pThrIleCysAspGlnAsnTrpLysAsnGluGlnAlaLeuValValVySCLysGlnLeuGl	411
q	1471		1530
οy	411		429
qq	1531	TCTGGGCTACGCCAACCACGGCCTGCAGGAGACCTGGTACTGGGACTCTGGGAATATAAC	1590
δ P	429	gaspleTrplleAsnSerlleSerCysThrGlyAsnGluSerAlaLeuTrpAspCysThis:::::::::::::::::::::::::::::::::::	449 .
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Sequence 1, Application US/09702572
Patent No. 6331602
GENERAL : FICKRAMITION:
GENERAL : FICKRAMITION:
TITLE OF INVENTION: USES THEREFOR
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: MNI-073
CURRENT APPLICATION NUMBER: US/09/702,572
CURRENT FILING DATE: 2000-10-31
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET: 2.0
                                                                                                   2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2057 -----CTCGAAGACACTGAGTGTCAGGAGGATGTCTCCAAGCGGTATGAGTGTGCCA 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GAGCAAGGCATCACTGTGGGTTGCTGGG 2144
                                   1651 CCATCATGGC---ACCCACATCACCTGCAAGAGGACAGGGACCCGCTTCACTGCTGGAGT 1707
                                                                                                                                                                                   ------GCACTGGTGCA-GGAGCCGCCTACA 1772
                                                                                                                                                                                                                                                                                                                                                                                                             1881 TCTCCTCCCAGATCCACAACCTGGGACGAGCTGACTTCAGGCCCAAGGCTGGGCGCCCACT 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CATGGGCATTACCACAGCA 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GCTGAGGGCCACA 2042
                                                                                                                                                                                                                                                                                                                                                                        -----IleGlyAsnGluS 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                550 erAsnIleTrp---AspCysGluHisSerGlyTrpGlyLysHisAsnCysValHisArgG 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 rpGlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaValValCysSerGlnL 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624 euAspCysProSerSerIleIleGlyMetGlyLeuGlyAsnAlaSerThrGlyTyrGlyL 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 ysIleTrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCysArgA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   664 snSerGlyTrpGlyAsnAsnAspCysSerHisSerGluAspValGlyVallleCysSerA 684
                                                                      111eCysSerAspLysAlaAspLeuAspLeuArgLeuValGlyAlaHisSerProCysTy 486
                                                                                                                                                  486 rGlyArgLeuGluValLysTyrGlnGlyGluTrpGlyThrValCysHisAspArgTrpSe 506
                                                                                                                                                                                                                          506 rThrArgAsnAla-----AlaValValCysLysGlnLeuGlyCysGlyLysProMe 523
                                                                                                                                                                                                                                                                                                  ...-HisValPheGlyMetThrTyrPheLysGluAlaSerGlyProIl 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                584 rgLeuValGlyGlySerAsnArgCysSerGlyArgLeuGluValTyrPheGlhGlyArgT 604
----ArgSerAspAlaGlyVa 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          569 luaspVal------IleValThrCysSerGlyAspAlaThrTrpGlyLeuA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684 sp-AlaSerAspMetGluLeuArgLeuValGlyGlySerSerArg 698
 449 rTyrAspGlyLysAlaLysArgThrCysPheArg--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2043 AAGCTAGTTTCTGT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 eTrpLeuAspAspVal-SerCys-----
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US-09-702-572-1
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SEQ ID NO 1
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LENGTH: 2920 TYPE: DNA ONGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (143)(2401)	Alignment Scores:  Pred. No.:  Score:  Score:  634.50  Matches:  2920  634.50  Matches:  214  40.038  Conservative:  77.548  Mismatches:  253  Query Match:  4 Roll Gaps:  2920  Antches:  214  Antches:  215  Best Local Similarity:  7.80%  Gaps:  215	59-130B-381 (1-1453) x US-09-702-572-1 (1-2920)	30 LeuLeuLeuAsnSerCysPheLeulleSerSerPheAsnGlyThr	45Glyasp 54	55 GlyProCysSerGlyThrValGluValLysPheGlnGlyGlnTrpGlyThrValCysAsp 74	AspGlyTrpAsnThrThrAlaSerThrValValCysLysGlnLeuGlyCysProPheSer 94	GAIGACTICACGCIGCCCAGGCIGCCCACACTCCICTGCCGGGGGCIGGGCTICACA 40 PheAla	10 GAGGCCACAGGCTGGACCCACAGTGCCAAATATGGCCCTGGAACAGGCCGC 46	110 IleTrpLeuAspAspValSerCysTyrGlyAsnGluSerAlaLeuTrpGluCysGlnHis 12: 	30 ArgGluTrpGlySerHisAsnCysTyrHisGlyGluAspValGlyValAsnCys 14	48TyrGlyGluAlaAsnLeu	81 CAGCGCCTCCCTGGCTTCTCGGACTCCAATGTCATTGAGGTAGAGCATCACCTGCAAGTG 64	54	SerCysSerGlyArgValGluValLysPheGlnGluArgTrpGlyThrIleCysAspAsp 18	2 GTGACGGAGGGCTGGTGGAAGTCAGGCTTCCTGACGGCTGGTCGCAAGTGTGCGACAAA	83 GlyTrpAsnLeuAsnThrAlaAlaValValCySArgGlnLeuGlyCysProSerSer 201	21	12 AGGGTCAACGC-GGCCTTCTACAGGCTGCTAGCCCAACGGCAGCAACACTCCTTTGGTCT 87	9 uAspAspIleLeuCysGlnGlyAsnGluLeuAlaLeuTrpAsnCysArgHisArgGlyTr 23	0.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	<pre>239 PG1YASDH126ASDCYSSETH1SASDG1UASDVALIDILLEUIDICCYS 234 31 FCGTGCCAATGACACCCCCAGGTGCCCTGGGGGGGGCCCTGCAGTGGTGAGCTGTGTGCC 990</pre>
LENG TYPE ORGP FEAT NAME LOCA	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	-09-7	3, 3,	2 4	<u>"</u> , %	, ,	ή ΄΄	4.1	11 94	13	14	38	15	16	9	7.	7(	8	21	ō 'n	93
`	Ali Pre SCC Per Per Que DBS	us.	QY Db	Qy Dp	δ, dd	8 8	oy Vo	qq	Oy Db	ζς Ω	δŏ	Q D	Oy Dp	Qy	q	G G	δy	QQ	Š Š	3 8	දු දු

Qy	255	TyrAspSerSer 258
qq	991	AGGCCCTGTCTACGCGGCATCCAGTGGCCAGAAGCAACAACAACAGTCGAAGCCTCAGGG 1050
Qy	25	AspLeuGluLeuArgLeuValGlyGlyThrAsnArgCysMetGlyArgValGluLeuLy 278
qq	2	GAGGCCCGTGTCCGTCTAAAGGGCGGCGCCCACCCTGGAGAGGCCGGGTAGAAGTCCT 11
δ,	278	IleGlnGlyArgTrpGlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaAspVa 298
Q	1111	11.
QY	298	1ValCysLysGlnLeuGlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGl 318
οy	. 318	alValTrpLeuAspGlyValSerCysSerGlyAsnGluSerPheLe 3
Dp	1231	
QY	338	uTrpaspCysArgHisSerGlyThrValAsnPheAspCysLeuHisGlnAsnAspValSe 358
qq	1291	
ΟY		37
qq	1351	TCGGGTGCAACCTACCTTACACTGGGGCAGAGACCAGGATCCGACTCAGTGGGGG
QY	375	rAsnAsnCysSerGlyArgValGluValArgIleHisGluGlnTrpTr 391
qq	1411	GCCAACATGAGGGCGAGTCGAGGTGCAAATAGGGGGACCTGGGCCCCTT
Qy	391	### ### ##############################
<b>q</b> 0 :	1471	SACCCTGGAGGCCATGGTGGCCTGTAGGCAACTGGG 15
Qy	411	7F
qq	1531	CTGGGCTACGCCAACCACGGCCTGCAGGAGACCTGGTACTGGGACT
ΟŊ	429	gAsplleTrplleAsnSerlleSerCysThrGlyAsnGluSerAlaLeuTrpAspCysTh 449
qq	1591	AGAGGTGGTGATGAGTGGAGTGCGCTGCAGGGACTGAGCTGTCCCTGGATCAGTGTGC 1650
Οy	449	TyraspGlyLysalaLysargThrCysPheargargSeraspalaGlyVa 466
qq	1651	ATCATGGC
Qy	466	Ti-
qq	1708	CTGTTCTGAGACTGCATCAGATCTGTTGCTG
QY	486	luValLysTyrGlnGlÿGluTrpGlyThrValC}
qq	1748	GCACTGGTGCA-GGAGACCGCCTACA 1772
Qy	206	sGln
qq	1773	TCGAAGACCGGCCCTGCATATGTTGTACTGTGCTGCGGAAGAAACT 1820
ΟŸ	523	тритугр
qa	1821	GCCTGGCCAGCTCAGCCCAACTGGCCCTATGGTCACCGGCGTCTGCTCCCGAT 1880
Qy	538	al-SerCysIleGlyAsnGlu
qq	1881	CTCCTCCCAGATCCACAACCTGGACGAGGTGACTTCAGGCCCAAGGCTG
δy	ĬŪ.	569
qq	1941	CCTGGGTGTGGCACGAGTGC

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pGlybe nGlyan :    GGGCC/ sSerG]	CCysAi			SnGly GATCT GATCT (GATCT (1 1   (TGGAG (1aSer (1aSe
aThrTrpGlyLeuA GGTG rPheGlnGlyArgT ::    -GCTGAGGGCCACA IValCysSerGlnL 	.uTrpSe ::: GTATGA YVall1 YVall1 TGTGGG		28720 386 183 501 629 80	erPher CTGTAC 1yThrV 1   1 GCCGAC hrThrP 1   CCAATC
ASPAL	Asple: Asple: AAGCGG ValG1: ATCAC' STATCAC' ATTAIG	Domain	1ve: 18 38 1ve: 18 50 80 -28720)	lesers   
SerGly :::    AATGGC LeuGlu LeuGlu AlaAla AlaAla GlyAsn	1yAspGluSerAspLeuTrpSerCysArgA 	CR	at at he	eLeuI
evalThrCysSerGlyAspAlaThrTrpGlyLeuA  :::     CCTCACCCCAAATGGCACCAAGGTG sSerGlyArgLeuGluValTyrPheGlnGlyArgT :::	31yAsp 	ng an 1,587 700096	Length: Matches: Conservat Mismatche Indels: Gaps:	rcysph 11 12 13 14 14 15 11 11 11 11 11 11 11 11 11 11 11 11
lleval Ill::: Arccrc CysSer CrpAsn frpAsn	CysAsp       GTCAG CysSer    JLeuVa  ::	1587 ntaini 709/34 1 1/DE98 9	09-341	uAsnSe :::: GGATGA 1AsnG1                 GAATGG CGTGTG SProPh
ratgati Asnargo	TrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCysArgA	S/0934. Jan ein Co ein Co 9-08-3 9-08-3 2-1	1.18e-45 618.50 33.638 22.818 7.608 4	1. Leule 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3. 3
CTCACT	spasp\ ::    shagack shagack shagack shagack shagack shagack shagack shagack	cation Us cons ON: nhauer, ON: Prote 110N NUMBI 10N NUMBI 1999 NTE: 1999 NOS: 12 In Ver.	1.18e-4 618.50 33.63% 22.81% 7.60% 4	######################################
al TCTTCP alGlyG alGlyG hrvalC ::   GTTTCI	rpLeuA             1       1       1     GA   SerAsp	Applicated 34606 (34606) (3460		ThrCys GACCTG LeuGlu III TTGGC GlnGly CAAGGG CysLys TGCAGG
luAspval	yslleTrpLeuAspAspValSerCysAspGlyAspGluSerAspLeuTrpSerCysArgA	587-7 7, 34p 10, 6346 10, 6346 10, 6346 11, 1006 11, 11, 1006 11, 11, 1006 11, 1006 12, 1006 13, 1006 14, 1006 15, 1006 16, 1006 17, 1006 18, 1006 19, 1006 10,	Scores: : imilarity: 1 Similarity ch: -130B-381 (1	ValValThrCysIleLeuLeuLeuAsnSerCysPheLeuIleSerSerPheAsnGly :::   ATTGTTGACCTCCTGGTGGGATGATGAAGGGTTCTTGTGTTCCCCTGTAGGATCTGAA ThrAspLeuGluLeuAsnGGATGAAGGGTTCTTGTGTTCCCTGTAGGATCTGAA ThrAspLeuGluLeuAsnGlyAspGlyProCySerGlyThrValGluVal :::
569 11980 2 2030 - 2043 1 624 4	2056 644 2057 664 2109 684	RESULT 12  'Sequence 7, Application US/09341587  Sequence 7, Application US/09341587  Sequence No. 6346606  GENERAL INFORMATION: APPLICANT: Mollenhauer, Jan TITLE OF INVENTION Protein Containing an SF FILE REFERENCE: 4121-108  CURRENT PILING DAFE: 1999-09-31  CURRENT FILING DAFE: 1999-01-09  SOFTWARE: PALLOTION NUMBER: PCT/DE98/00096  SOFTWARE: PALLOTION NUMBER: PCT/DE98/00096  SOFTWARE: PALCOTION NUMBER: PCT/DE98/00096  SOFTWARE: PCT/DE98/0009	nent No.: it S coca Mat Mat	25 2872 44 2932 64 2992 84
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Qy	101	GlyGlnalaValThrargHisGlyLysIleTrpLeuAspAspValSerCysTyrGlyAsn 120 
Qy	121 3163	GluseralareutrpGluCysGlnHisArgGluTrpGlySerHisAsnCysTyrHisGly 140
Qy Dp	141	GluAspvalGlyvalAsnCysTyrGlyGluAlaAsnLeuGly 154
οy	155	LeuArgLeuValAspGlyAsnAsn
qq	3283	TIGAAGTTTGCTCAGGAAGAAAATCCTAATTACATTCTGATCTCCTCACTCA
δλ	16	174
qq	3343	TCTTTATGAATTT 34
oy d	175	ArgTrpGlyThrileCysAspAspGlyTrpAsnLeuAsnThrAlaAlaValCysArg 194 :::
Qγ	19	PhelleSerSerGlyValValAsnSerProAla 212
QQ	3430	
δy	213	
qq	3489	AGTGCAAGGAAGAGAGAAAAAAAAAAGTGCTGGCTCCC3527
Qy	224	
qq	3528	CACGGCICCATITCIICCCIGCIGAGIAGCACIGGIIGAGGGIAICGIGGACACACAG 3584
οy	244	
QQ	3585	ACAGATAGCAGGGGGGGGGGGGTCCTCTCACTACAGGAACTGTGAACTAA-AGATGC 3643
QY	255	Tyraspserser
qq	3644	TTGTCTGGAAGTGGGTTCTCAGCTGAGACCCAGTGAGGGTCTGGAAATAGAGGCTCAA 3703
0у.	264	LeuvalGlyGlyThrAsnArgCysMetGlyArgValGluLeuLysIleGlnGlyArgTrp 283
QQ	3704	ŢĞŢ.
ογ	284	GlyThrValCysHisHisLysTrpAsnAsnAlaAlaAlaAspValValCysLysGlnLeu 303
qq	3748	GGAGTCCTTGACCTCAGGTCCTCTAAGAATGCTGCAGAGCACTGCCTGTGCCC-CAGGTC 3806
οy	304	GlyCysGlyThrAlaLeuHisPheAlaGlyLeuProHisLeuGlnSerGlySerAspVal 323
QQ	3807	GAGGCAGCCCCCATGAGT
δy	324	ValTrpLeuAspGlyValSerCysSerGlyAsnGluSerPheLeuTrpAspCys 341
g	3843	GCATGCCTTGTTATTGC 3860
δy	342	343
qq	3861	CTGTGGTCGGGGCTGTAAGATCACACAAGGCATTTGGGCTGGAGTGGCCTCCTCAGCCTT 3920
Qy	344	SerGlyThr
qq	3921	GCCAAAACATCCAAGGGAGAGTGTTGGTTTTGGGTCAA
QY	351	CysLeuHisGlnAsnAspValSerVallleCysSerAspGlyAlaAspLeuGlu 368
qq	3981	AATAGTGGCCAGGATC

፟.	369	LeuArgLeuAlaAspGlySerAsnAsnCysSerGlyArgValGluValArg1leHisGlu 388	
ā	4041	GCACCCCTTATA	
<u>≯</u>	389	-GloTrpTrpThrlacysAspGlnAsnTrpLysAsnGluGlnAl 403	
ą	4080		
¥	403	aLeuValValCysLysGlnLeuGlyCysProPheSerValPheGlySerArgArgAlaLy 423	
ą	4140		
<u>≻</u>	423	sProSerAsnGluAlaArgAspIleTrpIleAsnSerIleSerCysThrGlyAsnGluSe 443	
۵	4177	4016CATCTGATCTCTCTTTTTTTT	
<u>≻</u> ,	443	rAlaLeuTrpAspCysThrTyrAspGlyLysAlaLysArgThrCysPheArgSerAs 463	
۵	4210	CACAGCTGCTCAGTCCAGTCAACGCCCAGGCCAGGTGAGT 4250	
≽	463	PAlaGlyValIleCysSerAspLysAlaAspLeuAspLeuArgLeuValGlyAlaHisSe 483	
۵	4251	CCCCAGCATCCTTCATCGGGATGTCCCTTCTCTTTCTGCCCAGTTACCTCTTCCCCACTC 4310	
Δ	483	rProCysTyrGlyArgLeuGluVaLLys-TyrGlnGly	
۾	4311	CACAGAGCICTCCTGCTTTTCTGTGCGGATACTGTGGGGCATATTATTTTTCCTCCCACC 4370	
<u>≯</u> .	496	GluTrpGlyThrValCysHisAspArgTrpSerThrArgAsnAlaAlaV 51	
ð	4371		
Σ	512	alvalcys-LysGlnLeuGlyCysGlyLysProMetHisValPheGlyMetThrTyr 530	
ð	4431		
<u>&gt;</u> ,	531	PheLysGlualaSerGlyProIleTrpLeuAspAspValSerCysIleGlyAsnGluSer 550	
Q	4491		
λi	551	AsnIleTrpAspCysGluHis 557	
ą	4551	111 TG-ATACAACCTTTCTGAGAATTGAGAGTGACTGCCAAAGTCAC	
λ	558	SerGlyTrpGlyLysHisAsnCysValHisArgGluAspVallleVal 573	
ð	4610		
<u>X</u>	573	573	
ď	4670	CICCGICCCICACICCTICAAAIACCCCCAGAITITGCAAGGCCATAICTGCAICCAGAAA 4729	
X	574	ThrCysSerGlyAspAlaThrTrpGlyLeuArgLeu 585	
ą	4730	AGGCAGAG	
ζ	586	ValGly	
q	4790		
≿:	605	GlyThrValCysAspAspGlyTrpAsnSerLysAlaAlaAlaAlval 620	
Ð	4829		
λ	621	CysSerGlnLeuAsp-CysProSerSerIleIleGlyMetGlyLeuGlyAsnAla	
ą	4877		
⋩	640	rGlyTyrGlyLys1leTrpLeusspaspValSerCysAspGlyAspGl 656	
ą	4901		
ζ	959	uSerAspLeuTrpSerCysArgAsnSerGlyTrpGlyAsnAsnAspCysSerHi 674	

qa	4961	GAGGGATCGAACTGGTCTCCAGCAAGGCCTTTGTTCCTGGCTGTGCTCACT	5011
QY	674	sser-GluAspValGlyValIleCysSerAspAlaSerAspMetGluLeuArgLeuValG	694
qa	5012	GAGCTGAAGACTTGGGTAGCACTTGGAGCAAGTGGCAGGAACCAGAAATTGAATAGTTT-	5070
QY	694	lySerSerArgCysAlaGlyLysValGluValA	714
qa	5071		5101
δλ	714	euCysAla	716
qq	5102		5161
ΟŸ	717		
Dp	5162	ACTIGGCIGACCACCAACTIACCGGCAITGACAGIAGGIAAATAATCCICCTCGCCCTCC	5221
Qy	732	luCysGlySerAlalleArgValSerArgGluProH	744
QQ	5222	CTAGGGCTCACTCTACCTCTGGACAAACGTTTCTTTGAAAATGAAAGAATGAGGCTC	5281
QY	744	isPheThrGluArgThrLeuHisIleLeuMetSerAsnSerGly	758
qq	5282	CCTCT	5341
Qy	759		773
qq	5342	AACCTAGTCCTGGGTCAGATGTTGGAGGCTGGAGGTGGTGGTGACCTGTCTCCCCTGGG	5401
, oy	773	${ t sGlnThrAlaCysHisLeuAsnMetGlu}$	793
qq	5402		5425
QY	793	ILEuValGlyAlaAspMetProCysSerGlyArgValGluValLysHi 	813
qa	5426	!	5451
δλ	813	laAspThrTrpArgSerValCysAspSerAsp	83
qq	5452		5476
δλ	833		853
q <sub>Q</sub>	5477	TGGGACCTTGTTCCTGGCCCTCAGGCCACAGGCTGCAGACCTGCGAATAGTGGGGAAAG-	5535
QY	853	rTrpAlaGluLysPheGl	868
qq	5536		5562
δλ	868	luThrHisLeuAlaLeuCysProIleValGlnHis	888
qa	5563	TGTCCTACCATT	5596
Qy	888	rgGluValGlyValValCysSerArgTyrThrAspValArgLeuValAsnGlyLysSerG	806
qq	5597		5637
ΟY	806	lnCysAspGlyGlnValGluIleAsnValLeuGlyHisTrpGlySerLeuCysAspT	928
qq	5638		2667
QY	928	isTrpAspProGluAspAlaArgValLeuCysArgGlnLeuSerC)	948
qq	5668	AGCITCATCTGTGAG	5685
QY	948	erThrThrGlyGlyLysTyrIleGlyGluArgSerValArgValTrpG	964
qq	5686		5737
Oy	964	lyHisArgPheHisCysLeuGlyAsnGluSerLeuLeuAsp	. ' 226

Oy 1264 aGlySerTrpGlyThrVe :::         ::           ::	Oy 1321 eLeuTrpAsp  Db 6849 GTGTTGGGAGGGCAGCTTGGAGGGCAGCTTGGAGGGAGCAGCTTGGAGGAGGAGCAGCTTGGAGGTGAAGAGTGAAGAGTGAAGAGGTGAAGAGGTGAAGAGGTGAAGAGGTGAAGAGGTGAAGAGAGGAG	Qy 1355 aSerSerGlyHis Db 7023 CACATCCAGACAGAGG Qy 1361 aLeulleLeuSerSerI Db 7083 ATCCCTTATAAGGAGGG	944 X	APPLICANT: Wang, Allo APPLICANT: Casipit, C ITILE OF INVENTION: S, NUMBER OF EXQUENCES: CORRESPONDENCE ADDRESS ADDRESSE: Cetus On, STRÉET: 1400 Fifty- CITY: Emeryville STATE: CA COUMTRY: CA	REFFE	APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: FILING DATE: ATTORNEY/AGENT INFORMA' NAME: Goldman, Kenn REGISTRATION NUMBER: REFERENCE/DOCKET NUM TELECCMMUNICATION INFO TELECCMMUNICATION INFO TELECHNONE: (510) 658-
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978 GTCACAGGTGCTTCCCCAATACTTGAGCTTCCATAGACTTGGGTGGAGTAGGAC 5791 978ASnCys-GlnMetThrValleuGlyAlaProProCysIleHisGlyAsnThrValSer 996 :::	1026 rAlaLeuIleCysLeuGluAspLysArgLeuArgLeuValAspGlyAspSerArgCysAl	6077 CACCAATGAGCCAATGTGGACCAGGCAGGGCTGGGCTGG	1126 6257 1146 6288	1166 rvalGlyArgArgAsn	6448 CCTAGTGTTCCTGTGGTCACTTAGGACAGGGACCAAACTGAAACAACCCCGGACTTT 6507   1194	1211 nCysProLysThrHisIle
0	oy oy	40 da 60 da .	9 9 9 9	64 65 65 65 65 65 65 65 65 65 65 65 65 65	qa 66 qa	0

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1091 PheGlyGluGlySerGlyProIleTrpLeuAspAspLeuAsnCysThrGlyThrGluSer 1110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1191 ValValSerLeuAlaProLeuSerLySThrGlySerGlyPheMetTrpValAspAspIle 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 GlnCysProLysThrHisIleSerIleTrpGlnCysLeuSerAlaProTrpGluArgArg 1230
                                                                                                                                                                                                                                                                                                                                                                  1031 LeuGluAspLysArgLeuArgLeuValAspGlyAspSerArgCysAlaGlyArgValGlu 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                         IleTyrHisAspGlyPheTrpGlyThrIleCysAspAspGlyTrpAspLeuSerAspAla 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisValValCysGlnLysLeuGlyCysGlyValAlaPheAsnAlaThrValSerAlaHis 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1131 AlaGlyValIleCysSerGluPheThrAlaLeuArgLeuTyrSerGluThrGluThrGlu 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1151 SerCysAlaGlyArgLeuGluValPheTyrAsnGlyThrTrpGlySerValGlyArgArg 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1171 AsnIleThrThrAlaIleAlaGlyIleValCysArgGlnLeuGlyCysGlyGluAsnGly 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1231 IleSerSerProAlaGluGluThrTrpIleThrCysGluAspArgIleArgValArgGly 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TrpHisAlaGlySerTrpGlyThrValCys 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 GCTGGTCTGCACCAATGAAACC------AGGAGCACCCACACCCTG 578
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                                                                                                                                                                                                                                                                                                                              US-09-759-130B-381 (1-1453) x US-08-477-674-9 (1-2285)
                                                                                                                                                                                                                                        Conservative:
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Indels:
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Matches:
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ATTGACATCACCTGTCGTCAGTCAAGTGCTTCCAC-
             INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                  3.56e-19
                                                                                                                                                                                                                   314.00
42.00%
30.57%
3.86%
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                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                             US-08-477-674-9
TELEX:
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6-	INFORMATION SEQUENCE C LENGTH: TYPE: TYPE: TOPOLOGY MOLECULE T S-08-473-791-9	I INFORMATION THE RENDETH IN WINDER: 34 OCKET NUMBER: 1100 INFORMATION (510) 420-31
man, Kenneth M.  N NUMBER: 34,174  OCKET NUMBER: 2595.  OCKET NUMBER: 2595.  (510) 420-3152  510) 658-5470  SEQ ID NO: 9:  AGTERISTICS: 85 base pairs sic acid 5: single 5: single 5: Dinar 5: Dinar 6: Dinar 7: D	Menneth M. ABER: 34,174 I NUMBER: 2595. INFORMATION: ) 420-3152 658-5470	MODEL AND THE OWNER THE OW
NUMBER: US/08  "UNMBER: US/07  "IS-CCT-1992  IINFORMATION: N UNMBER: 34,1  COKET NUMBER: 110N INFORMATION  SEQ ID NO: 9: ATTERISTICS: 85 base pairs and a strong a st	JER: US/08/316, JER: US/07/961, OCMMATION: Kenneth M. HER: 34,174 F NUMBER: 2595, INFORMATION: 1 NUMBER: 2595, 1 NUMBATION: 0,420-3152	US/08/316, US/07/961, T-1992
CATTON DATA:  COMMBER: US/08/473,  1008. 435  TION: 435  TION DATA:  NUMBER: US/08/316,  15-0CT-1992  TINFORMATION:  NUMBER: 34,174  NUMBER: 34,174  NUMBER: 2595  TINFORMATION:  NUMBER: 2595  TOKET NUMBER:	NN DATA: NN DATA: 1-JUN-1995 435 DATA: BER: US/08/316, SER: US/07/961, SER: US/08/316, SER: US	S/08/473, 995 S/08/316, S/07/961, 992
ABLE FORM:  Floppy disk  Floppy disk  Formatible  FORMS-DOS/MS-DO  PATION DATA:  NUMBER: US/08/473,  TION DATA:  NUMBER: US/08/316,  IS-COT-1992  TINFORMATION:  IS-COT-1992  TINFORMATION:  IS-COT-1992  TINFORMATION:  SEC ID NO: 9:  ACTERISTICS:  SED ID NO: 9:  ACTERISTICS:  SED ASP PAIRS  SINGLE  LINEAR  SEL SINGLE	FORM:	SIMIR: CA ZIP: 94608 MPUTER READABLE FORM: MPUTER READABLE FORM: COMPUTER: IBM PC COMPATIBLE ODERATING SYSTEM: PC-TOS/MS-DOS OSTWARRE: PATENTING NUMBER: US/08/473,791 APPLICATION NUMBER: US/08/473,791 CLASSIFICATION 1995 CLASSIFICATION 1995 TING DATE: US/08/316,714 FILING DATE: US/08/316,714 FILING DATE: 15-OCT-1992
UENCES: 11 E ADDRESS: E ADDRESS: OCCUEUS ONCOLOGY CORPORATION OO Fifty-Third Street Yille SA ABLE FORM: Floppy disk ISPACE COMPATIBLE COMPATIBLE ONTON DATA: ON-JUN-1995 ION: 435 ION: 435 ION: 435 ION: 435 ION: A35 ION: A35 ION: A35 ION: A35 ION: A35 ION: A35 ION: BATA: ONT-JUN-1995 ION: A35 ION: BATA: ION DATA: ION DATA: ION DATA: SECTION OF STREET STREET SECTION: ION WHERE: 2595.1 ION NABER: 2595.1 ION NABER: 2595.1 ION BATA: SECTION OF STREET STREET SECTION OF STRE	SS: 11  SESS:  SONCOLOGY CORPORATION  Ifty-Third Street  COMPATION  FORM:  COMPATION:  -JUN-1995  A35  DATA:  -JUN-1995  A45  BER: US/08/473,791  -JUN-1995  COMMATION:  KENDER: MANDER:  SER: US/08/316,714  SER: US/08/316,714  SER: US/08/316,714  SER: US/07/961,404  COMMATION:  MUMBER: 2595.1  INFORMATION:  1 A20-3152  658-5470	MBER OF SEQUENCES: 11  ADDRESSES: RESPONDENCE ADDRESS:  ADDRESSE: 1400 Fifty-Third Street  CITY: Emeryville  STREET: 1400 Fifty-Third Street  CITY: Emeryville  COUNTRY: USA  COUNTRY: USA  MUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  MEDIUM TYPE: TOWN DATA:  SOFTWARE: PRECENTION NUMBER: US/08/473,791  FILLING DATE:  APPLICATION NUMBER: US/08/416,714  APPLICATION NUMBER: US/07/961,404  FILLING DATE: 15-OCT-1992
trans.  tron.  t	14 473-791-9 ence 9, Application US/08473791. nt No. 5736340 ERAL INFORMATION: ERAL INFORMATION: EPLICANT: Koths, Kirston E. PPLICANT: Taylor, Eric W. PPLICANT: Taylor, Eric W. PPLICANT: Gasipit, Clayton L. ITLE OF INVENTION: Secreted Mac-2-Binding OWBER OF SEQUENCES: 11 OWBER OF SEQUENCES: 11 OWBER OF SEQUENCES: 11 OWBERSEE: Cetus Oncology Corporation STREET: 1400 Fifty-Third Street CITY: Emeryville STREET: 1400 Fifty-Third Street COUNTRY: USA LIP: 94608 OMBUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version APPLICATION NUMBER: US/08/473,791 FILING DATE: 07-1995 TILING DATE: 15-OCT-1992 TTORNEY/AGENT INFORMATION: RAPLICATION NUMBER: US/08/316,714 APPLICATION NUMBER: US/08/316,714	14 473-791-9 nt No. 5736340 nt No. 5736340 ERAL INFORMATION ERAL INFORMATION ERAL INFORMATION EPLICANT: Halenbeck, Robert F. PPLICANT: Halenbeck, Robert F. PPLICANT: Haylor, Eric W. PPLICANT: Anylor, Ent W. PPLICANT: Wang, Alice M. ITLE OF INVENTION: Secreted Mac-2-Binding ORRESPONDENCE ADDRESS: ADDRESSEE: Cetus Oncology Corporation STREET: 1400 Fifty-Third Street COUNTY: Emeryville STREET: A. STREET: A. STREET: A. STREET: A. STREET: A. STREET: B. OWBUTER: PROBABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version APPLICATION NUMBER: US/08/473,791 FILING DATE: US/08/316,714 FILING DATE: US/08/316,714 FILING DATE: US/07-1992 APPLICATION NUMBER: US/08/316,714 FILING DATE: 15-OCT-1992
349 SerLeuLysSerLeuAsnalaSerSerGly 1358	1349 SerLeuLysSerLeuAsnalaSerSerGly 1358  1014 GAACTTCGAGCCCTGACGCAGGCCAGGC 1063  SGULT 14  SEQUENCE 9, Application US/08473791.  PAPLICANT: Halenbeck, Robert F.  APPLICANT: Halenbeck, Robert F.  APPLICANT: Halenbeck, Robert F.  APPLICANT: Halenbeck, Robert F.  APPLICANT: Gasipit, Clayton L.  APPLICANT: Gasipit, Clayton L.  TILE OF INVENTION: Secreted Mac-2-Binding NUMBER OF SEQUENCES: 11  CORRESPONDENCE ADDRESS: ADDRESSEE: CALUS OCOLOGY Corporation STREET: 1400 Fifty-Third Street  CITY: Emeryville  STREET: 1400 Fifty-Third Street  CONFUTRY: USA  ZIP: 94608  COMPUTER: Floppy disk  COMPUTER: EMPRYVILLE  STREET: 1400 Fifty-Third Street  CONFUTRY: USA  ZIP: 94608  COMPUTER: ADDRESSEE COMPORTER  MEDIUM TYPE: Floppy disk  COMPUTER: ADDRESSEE OF COMPORTER  MEDIUM TYPE: Floppy disk  COMPUTER: DATE: 07-UN-1995  SCFTWARE: PatentIn Release #1.0, Version  CURSENT APPLICATION NUMBER: US/08/473,791  FILING DATE: 07-UN-1995  ATTORN APPLICATION NUMBER: US/08/316,714  FILING DATE: 15-OCT-1992  ATTORN APPLICATION NUMBER: 34,174  REGISTRATION NUMBER: 34,174  REGISTRATION NUMBER: 34,174  REGISTRATION NUMBER: 34,174  REFERENCE/DOCKET NUMBER: 34,174	1349 SerLeuLysSerLeuAsnalaSerSerGly 1358        :::       :::
1329 ProTrpGlyGlnSerAspCysGlyHisLysGluAspala  1349 CCTGCTGGA	1329 ProTrpClyGlnSerAspCysGlyHisLysGluAspAlaGlyValArgCysSerGlyGln 998 CCTGCTGGA. 1349 ScTCeutySerLeuAsnAlaSerSerGly 1358 1139 SerLeuLySGerLeuAsnAlaSerSerGly 1358 1134 GAACTTCGAGGCCTTGACGCAGGCCGAGGC 1063 SGULT 14 1034 GAACTTCGAGGCCTTGACGCAGGCCGAGGC 1063 SGULT 14 1034 GAACTTCGAGCCTTGACGCAGGCCGAGGC 1063 SGULT 14 1054 APPLICANT: Halenbeck, Robert F. APPLICANT: Taylor, Eric W. APPLICANT: Taylor, Eric W. APPLICANT: Taylor, Eric W. APPLICANT: Taylor, Secreted Mac-2-Binding Glycoprotein NUMBER OF SEQUENCES: 1 1406 Fifty-Third Street 1407 Fifty-Third Street 1407 Fifty-Third Street 1406 Fifty-Third Street 1407 Fifty-Third Street	1329 ProTrpGlyGlnSerAspcysGlyHisLysGluAspAlaGlyValArgCysSerGlyGln 1329 ProTrpGlyGlnSerAspcysGlyHisLysGluAspAlaGlyValArgCysSerGlyGln 1349 SerLeuLysSerLeuAsnAlaSerSerGly 1358 111::::
1309 TrpLeuaspaspwetargCysLysGlyAsnGluSerPheLeuTrpAspCysHisAlaLys 971 TGCCIM	1309 TrpLeuAspaspWetArgCysLysGlyAsnGluSerPheLeuTrpAspCysHishlaLys 971 TGCTA	1309 TrpLeudspaspWetArgCysLysGlyasnGluSerPheLeuTrpAspCysHisAlaLys
1291 SerAlaLeuwlaalalaLeu	1291 Seralateualaalalaeu	1291 SerAlaLeuAlaAlaLeuArgAspAlaSerPheGlyGlnGlyThrIle 11912 AGCTGTTGCCATCCTCCCCCGGGCCCTGTA 1309 TrpLeuAspAspAlesGrCCTGCTCCTCCTCCTCGTCCTGTA 1309 TrpLeuAspAspMetArgCysLyGlyAsnGluSerPheLeuTrpAspCysHisAlaLyS 1309 TrpLeuAspAspMetArgCysLyGlyAsnGluSerPheLeuTrpAspCysHisAlaLyS 1310 TrpLeuAspAspMetArgCysLyGlyAsnGluSerPheLeuTrpAspCysHisAlaLyS 1311 GCCTA

1349 SerLeuLysSerLeuAsnAlaSerSerGly 1358

Best La Query 1 DB:	t Local Similarity: 30.57% Mismatches: 108 ry Match: 3.86% Indels: 96 1 Gaps: 15	
ns-c	-09-759-130B-381 (1-1453) x US-08-473-791-9 (1-2285)	
oy Q	1031 LeuGluAspLysArgLeuArgLeuValAspGlyAspSerArgCysAlaGlyArgValGlu 1050 :::     :::	
Oy Dp	3 1	
Qy Db	1	
oy op	1091 PheGlyGluGlySerGlyProIleTrpLeuAspAspLeuAsnCysThrGluSer 1110	
oy og	1111 HisLeuTrpGlnCysProSerArgGlyTrpGlyGlnHisAspCysArgHisLysGluAsp 1130	
Oy Dp	1131 AlaGlyValileCysSerGluPheThrAlaLeuArgLeuTyrSerGluThrGluThrGlu 1150	:
Qy Db	1151 SerCysAlaGlyArgLeuGluValPheTyrAsnGlyThrTrpGlySerValGlyArgArg 1170 ::: 579 GACCTCTCCAGG 590	•
9 o	1171 ASNITETHITHIAIALILEALAGIYILEVALCYSAIGGINLEUGIYCYSGIYGIUASNGIY 1190	
Qy Dp	1191 ValValSerLeuAlaProLeuSerLysThrGlySerGlyPheMetTrpValAspAspIle 1210 :::   :::	
07 DP	1211 GlnCysProLysThrHisIleSerIleTrpGlnCysLeuSerAlaProTrpGluArgArg 1230 	
oy g	1231 IleSerSerProAlaGluGluThrTrpIleThrCysGluAspArgIleArgValArgGly 1250	
Oy Dp	1251 GlyaspThrGluCys	
Qy Db	1259 ValGluileTrpHisAlaGlySerTrpGlyThrValCys 1271 ::::	
oy op	1272 AspAspSerTrpAspLeuAlaGluAlaGluValValCysGlnGlnLeuGlyCysGly 1290 	
oy op	1291 SeralaLeualaalaLeuArgaspalaSerPheGlyGlnGlyThrGlyThrIle 1308	
oy op	1309 TrpLeuAspAspMetArgCysLysGlyAsnGluSerPheLeuTrpAspCysHisAlaLys 1328 	
S S	1329 ProfrpGlyGlnSerAspCysGlyHisLysGluAspAlaGlyValArgCysSerGlyGln 1348 	

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1071 HisValValCysGlnLysLeuGlyCysGlyValAlaPheAsnAlaThrValSerAlaHis 1090
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US-08-316-714-9
; Sequence 9, Application US/08316714
; Patent No. 5965382
; GENERAL INFORMATION:
    APPLICANT: Koths, Kirston E.
    APPLICANT: Halenbeck, Robert F.
    APPLICANT: Taylor, Eric W.
    APPLICANT: Taylor, Eric W.
    APPLICANT: Gasipit, Clayton L.
    TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
    NUMBER OF SEQUENCES: 11
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,714
FILING DATE:
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                ADDRESSEE: Cetus Oncology Corporation
STREET: 1400 Fifty-Third Street
CITY: Emeryville
1034 GAACTTCGAGGCCTTGACGCAGGCCGAGGC 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/961,404
FILING DATE: 15-007-1992
ATTOMNEY AGENT INFORMATION:
NAME: GOLDMAN, KENNETH M.
REGISTRATION NUMBER: 34,174
REFERNCE/DOCKET NUMBER: 2595.1
TELEPHONE: (510) 420-3152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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314.00
42.00%
30.57%
3.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2285 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
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Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                     CITY: EMC
STATE: CACOUNTRY:
qq
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QQ	354	AGCGTCGTCTGCCGGGCCCTGGGCTTCGAGAACGCCACCCAGGCTCTGGGCAGAGCTGCC 413	
Qy	1091	PheGlyGluGlySerGlyProIleTrpLeuAspAspLeuAsnCysThrGlyThrGluSer 1110	0
qa	414	TTCGGGCAAGGATCAGGCCCCATCATGCTGGACGAGGTCCAGTGCAGGGAACCGAGGCC 473	
Oy	1111	HisLeuTrpGlnCysProSerArgGlyTrpGlyGlnHisAspCysArgHisLysGluAsp 113	0
qa	474	TCACTGGCCGACTGCAAGTCCCTGGGCTGGCTGAAGAGCAACTGCAGGCACGAGAGAGA	
QY	1131	AlaGlyValIleCysSerGluPheThrAlaLeuArgLeuTyrSerGluThrGluThrGlu 1150	0
q	534	GCTGGTGTGGTCTGCACCAATGAAACCAGGAGCACCACACCCTG 578	
QY	1151	SerCysAlaGlyArgLeuGluValPheTyrAsnGlyThrTrpGlySerValGlyArgArg 1170	.0
qa	579	GACCTCTCCAGG 590	
Qy	1171	AsnIleThrThrAlaIleAlaGlyIleValCysArgGlnLeuGlyCysGlyGluAsnGly 119	. 0
đ	591		
Οy	.1191	ValValSerLeuAlaProLeuSerLysThrGlySerGlyPheMetTrpValAspAspIle 121	0
q	648	:::   ::: ATCAGCGTGAATGTGCCAGGCGGAGGACGCCCTGGGCTTC	
٥y	1211	GlnCysProLysThrHisIleSerIleTrpGlnCysLeuSerAlaProTrpGluArgArg 123	
qq	687	TGTGGCCACACGGTCATC	
QY	1231	IleSerSerProAlaGluGluThrTrpIleThrCysGluAspArgIleArgValArgGly 1250	0
qa	723	111 111 111 111 111 111 111 111 111 11	
Qy	1251	GlyAspThrGluCysSerGlyArg 125	8
qq	168		
ΟŊ	1259	ValGlulleTrpHisAlaGlySerTrpGlyThrValCys 1271	
qq	828		
QY	1272	AspAspSerTrpAspLeuAlaGluAlaGluValValCysGlnGlnLeuGlyCysGly 129	0
d G	864		
ΟŊ	1291	SerAlaLeuAlaAlaLeuArgAspAlaSerPheGlyGlnGlyThrGlyThrIle 130	89
đ	912		
Qy	1309	TrpLeuAspAspMetArgCysLysGlyAsnGluSerPheLeuTrpAspCysHisAlaLys 132	8
qq	971	TGCCTAAGGGGACGC 997	
Qy	1329	ProTrpGlyGlnSerAspCysGlyHisLysGluAspAlaGlyValArgCysSerGlyGln 134	8
qq	866	CTGCTGGAGAAGCTCTGCCTACAGTTCCTGGCCTG 103	8
Qy.	1349	SerLeuLysSerLeuAsnAlaSerSerGly 1358	•
QQ	1034		:
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